

SEQUENCE LISTING

5 <110> KUEHN, Ralf
FELDER, Susanne
SCHWENK, Frieder
KUETER-LUKS, Birgit
FAUST, Nicole

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<220>
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50 <220>
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 cagctggcac gacagtttcc cgactggaa agcgggcagt gaggcgaacg caattatgt 6120
 gagttagctc actcattagg caccggcggc tttacacttt atgcttccgg ctcgtatgtt 6180
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 <223> Description of Artificial Sequence: primer P64-1

30 <400> 17
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<210> 18
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 35 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: primer 64-4

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 gacgacagta tcggcctcag gaagatc 27

45 <210> 19
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 oligonucleotide 80d

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 gggcactact cccgaaaacc gcttctggat ccataacttc gtatagcata cattatacga 480
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25	aca cag cgt agc gcc aac gaa gac aag gcg gcc gac ctt cag cgc gaa Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu 35 40 45	144
30	gtc gag cgc gac ggg ggc cgg ttc agg ttc gtc ggg cat ttc agc gaa Val Glu Arg Asp Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu 50 55 60	192
35	gcg ccg ggc acg tcg gcg ttc ggg acg gcg gag cgc ccg gag ttc gaa Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu 65 70 75 80	240
40	cgc atc ctg aac gaa tgc cgc gcc ggg cgg ctc aac atg atc att gtc Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val 85 90 95	288
45	tat gac gtg tcg cgc ttc tcg cgc ctg aag gtc atg gac gcg att ccg Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro 100 105 110	336
50	att gtc tcg gaa ttg ctc gcc ctg ggc gtg acg att gtt tcc act cag Ile Val Ser Glu Leu Ala Leu Gly Val Thr Ile Val Ser Thr Gln 115 120 125	384
55	gaa ggc gtc ttc cgg cag gga aac gtc atg gac ctg att cac ctg att Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile 130 135 140	432
60	atg cgg ctc gac gcg tcg cac aaa gaa tct tcg ctg aag tcg gcg aag Met Arg Leu Asp Ala Ser His Lys Glu Ser Ser Leu Lys Ser Ala Lys 145 150 155 160	480
65	att ctc gac acg aag aac ctt cag cgc gaa ttg ggc ggg tac gtc ggc Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly 165 170 175	528
70	ggg aag gcg cct tac ggc ttc gag ctt gtt tcg gag acg aag gag atc Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile 180 185 190	576
75	acg cgc aac ggc cga atg gtc aat gtc gtc atc aac aag ctt gcg cac Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His 195 200 205	624
80	tcg acc act ccc ctt acc gga ccc ttc gag ccc gac gta atc Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile	672

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10	ccg ggc agt caa gcc gcc att cac ccg ggc agc atc acg ggg ctt tgt Pro Gly Ser Gln Ala Ala Ile His Pro Gly Ser Ile Thr Gly Leu Cys 245 250 255			768
15	aag cgc atg gac gct gac gcc gtg ccg acc ccg ggc gag acg att ggg Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly 260 265 270			816
20	aag aag acc gct tca agc gcc tgg gac ccg gca acc gtt atg cga atc Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile 275 280 285			864
25	ctt ccg gac ccg cgt att gcg ggc ttc gcc gct gag gtg atc tac aag Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys 290 295 300			912
30	aag aag ccg gac ggc acg ccg acc acg aag att gag ggt tac cgc att Lys Lys Pro Asp Gly Thr Pro Thr Lys Ile Glu Gly Tyr Arg Ile 305 310 315 320			960
35	cag cgc gac ccg atc acg ctc ccg gtc gag ctt gat tgc gga ccg Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro 325 330 335			1008
40	atc atc gag ccc gct gag tgg tat gag ctt cag gcg tgg ttg gac ggc Ile Ile Glu Pro Ala Glu Trp Tyr Glu Leu Gln Ala Trp Leu Asp Gly 340 345 350			1056
45	agg ggg cgc ggc aag ggg ctt tcc ccg ggg caa gcc att ctg tcc gcc Arg Gly Arg Gly Lys Gly Leu Ser Arg Gly Gln Ala Ile Leu Ser Ala 355 360 365			1104
50	atg gac aag ctg tac tgc gag tgt ggc gcc gtc atg act tcg aag cgc Met Asp Lys Leu Tyr Cys Glu Cys Gly Ala Val Met Thr Ser Lys Arg 370 375 380			1152
55	ggg gaa gaa tcg atc aag gac tct tac cgc tgc cgt cgc ccg aag gtg Gly Glu Glu Ser Ile Lys Asp Ser Tyr Arg Cys Arg Arg Arg Lys Val 385 390 395 400			1200
60	gtc gac ccg tcc gca cct ggg cag cac gaa ggc acg tgc aac gtc agc Val Asp Pro Ser Ala Pro Gly Gln His Glu Gly Thr Cys Asn Val Ser 405 410 415			1248
65	atg gcg gca ctc gac aag ttc gtt gcg gaa cgc atc ttc aac aag atc Met Ala Ala Leu Asp Lys Phe Val Ala Glu Arg Ile Phe Asn Lys Ile 420 425 430			1296
70	agg cac gcc gaa ggc gac gaa gag acg ttg gcg ctt ctg tgg gaa gcc Arg His Ala Glu Gly Asp Glu Glu Thr Leu Ala Leu Leu Trp Glu Ala 435 440 445			1344
75	gcc cga cgc ttc ggc aag ctc act gag gcg cct gag aag acg ggc gaa Ala Arg Arg Phe Gly Lys Leu Thr Glu Ala Pro Glu Lys Ser Gly Glu 450 455 460			1392
80	cgg gcg aac ctt gtt gcg gag cgc gcc gac gcc ctg aac gcc ctt gaa Arg Ala Asn Leu Val Ala Glu Arg Ala Asp Ala Leu Asn Ala Leu Glu 465 470 475 480			1440
85	gag ctg tac gaa gac cgc gca ggc gcg tac gac gga ccc gtt ggc			1488

Glu Leu Tyr Glu Asp Arg Ala Ala Gly Ala Tyr Asp Gly Pro Val Gly
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5 agg aag cac ttc cgg aag caa cag gca gcg ctg acg ctc cgg cag caa 1536
 Arg Lys His Phe Arg Lys Gln Gln Ala Ala Leu Thr Leu Arg Gln Gln
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10 ggg gcg gaa gag cgg ctt gcc gaa ctt gaa gcc gcc gaa gcc ccg aag 1584
 Gly Ala Glu Glu Arg Leu Ala Glu Leu Glu Ala Ala Glu Ala Pro Lys
 515 520 525

15 ctt ccc ctt gac caa tgg ttc ccc gaa gac gcc gac gct gac ccg acc 1632
 Leu Pro Leu Asp Gln Trp Phe Pro Glu Asp Ala Asp Ala Asp Pro Thr
 530 535 540

20 ggc cct aag tcg tgg tgg ggg cgc gcg tca gta gac gac aag cgc gtg 1680
 Gly Pro Lys Ser Trp Trp Gly Arg Ala Ser Val Asp Asp Lys Arg Val
 545 550 555 560

25 ttc gtc ggg ctc ttc gta gac aag atc gtt gtc acg aag tcg act acg 1728
 Phe Val Gly Leu Phe Val Asp Lys Ile Val Val Thr Lys Ser Thr Thr
 565 570 575

30 ggc agg ggg cag gga acg ccc atc gag aag cgc gct tcg atc acg tgg 1776
 Gly Arg Gly Gln Gly Thr Pro Ile Glu Lys Arg Ala Ser Ile Thr Trp
 580 585 590

35 gcg aag ccg ccg acc gac gac gac gaa gac gac gac gcc cag gac ggc acg 1824
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40 gaa gac gta gcg gcg tag 1842
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 <213> Bacteriophage phi-C31

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60 Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu
 35 40 45

Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu
 50 55 60

65 Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu
 65 70 75 80

70 Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val
 85 90 95

75 Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro
 100 105 110

80 Ile Val Ser Glu Leu Leu Ala Leu Gly Val Thr Ile Val Ser Thr Gln
 115 120 125

85 Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile

130 135 140

Met Arg Leu Asp Ala Ser His Lys Glu Ser Ser Leu Lys Ser Ala Lys
 145 150 155 160

5 Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly
 165 170 175

10 Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile
 180 185 190

Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His
 195 200 205

15 Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile
 210 215 220

Arg Trp Trp Trp Arg Glu Ile Lys Thr His Lys His Leu Pro Phe Lys
 225 230 235 240

0 Pro Gly Ser Gln Ala Ala Ile His Pro Gly Ser Ile Thr Gly Leu Cys
 245 250 255

5 Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly
 260 265 270

Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile
 275 280 285

10 Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys
 290 295 300

15 Lys Lys Pro Asp Gly Thr Pro Thr Thr Lys Ile Glu Gly Tyr Arg Ile
 305 310 315 320

20 Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro
 325 330 335

25 Ile Ile Glu Pro Ala Glu Trp Tyr Glu Leu Gln Ala Trp Leu Asp Gly
 340 345 350

30 Arg Gly Arg Gly Lys Gly Leu Ser Arg Gly Gln Ala Ile Leu Ser Ala
 355 360 365

35 Met Asp Lys Leu Tyr Cys Glu Cys Gly Ala Val Met Thr Ser Lys Arg
 370 375 380

Gly Glu Glu Ser Ile Lys Asp Ser Tyr Arg Cys Arg Arg Arg Lys Val
 385 390 395 400

40 Val Asp Pro Ser Ala Pro Gly Gln His Glu Gly Thr Cys Asn Val Ser
 405 410 415

45 Met Ala Ala Leu Asp Lys Phe Val Ala Glu Arg Ile Phe Asn Lys Ile
 420 425 430

50 Arg His Ala Glu Gly Asp Glu Glu Thr Leu Ala Leu Leu Trp Glu Ala
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55 Ala Arg Arg Phe Gly Lys Leu Thr Glu Ala Pro Glu Lys Ser Gly Glu
 450 455 460

60 Arg Ala Asn Leu Val Ala Glu Arg Ala Asp Ala Leu Asn Ala Leu Glu
 465 470 475 480

65 Glu Leu Tyr Glu Asp Arg Ala Ala Gly Ala Tyr Asp Gly Pro Val Gly
 485 490 495

Arg Lys His Phe Arg Lys Gln Gln Ala Ala Leu Thr Leu Arg Gln Gln
 500 505 510

5 Gly Ala Glu Glu Arg Leu Ala Glu Leu Glu Ala Ala Glu Ala Pro Lys
 515 520 525

Leu Pro Leu Asp Gln Trp Phe Pro Glu Asp Ala Asp Ala Asp Pro Thr
 530 535 540

10 Gly Pro Lys Ser Trp Trp Gly Arg Ala Ser Val Asp Asp Lys Arg Val
 545 550 555 560

15 Phe Val Gly Leu Phe Val Asp Lys Ile Val Val Thr Lys Ser Thr Thr
 565 570 575

Gly Arg Gly Gln Gly Thr Pro Ile Glu Lys Arg Ala Ser Ile Thr Trp
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<211> 1863

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<220>

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 coding for fusion protein C31-Int(CNLS)

<220>

<221> CDS

40 <222> (1)...(1860)

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 Asp Arg Gln Ser Arg Glu Arg Glu Asn Ser Ser Ala Ala Ser Pro Ala
 20 25 30

50

aca cag cgt agc gcc aac gaa gac aag gcg gcc gac ctt cag cgc gaa
 Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu
 35 40 45

55

gtc gag cgc gac ggg ggc cgg ttc agg ttc gtc ggg cat ttc agc gaa
 Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu
 50 55 60

60

gcg ccg ggc acg tcg gcg ttc ggg acg qcg gag cgc ccg gag ttc gaa
 Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu
 65 70 75 80

65

cgc atc ctg aac gaa tgc cgc gcc ggg cgg ctc aac atg atc att gtc
 Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val
 85 90 95

tat gac gtg tcg cgc ttc tcg cgc ctg aag gtc atg gac gcg att ccg
 Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro
 336

48

96

144

192

240

288

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10	gaa ggc gtc ttc cgg cag gga aac gtc atg gac ctg att cac ctg att Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile 130 135 140			432
15	atg cgg ctc gac gcg tcg cac aaa gaa tct tcg ctg aag tcg gcg aag Met Arg Leu Asp Ala Ser His Lys Glu Ser Ser Leu Lys Ser Ala Lys 145 150 155 160			480
20	att ctc gac acg aag aac ctt cag cgc gaa ttg ggc ggg tac gtc ggc Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly 165 170 175			528
25	ggg aag gcg cct tac ggc ttc gag ctt gtt tcg gag acg aag gag atc Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile 180 185 190			576
30	acg cgc aac ggc cga atg gtc aat gtc gtc atc aac aag ctt gcg cac Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His 195 200 205			624
35	tcg acc act ccc ctt acc gga ccc ttc gag ttc gag ccc gac gta atc Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile 210 215 220			672
40	cgg tgg tgg tgg cgt gag atc aag acg cac aaa cac ctt ccc ttc aag Arg Trp Trp Trp Arg Glu Ile Lys Thr His Lys His Leu Pro Phe Lys 225 230 235 240			720
45	ccg ggc agt caa gcc gcc att cac ccg ggc agc atc acg ggg ctt tgt Pro Gly Ser Gln Ala Ala Ile His Pro Gly Ser Ile Thr Gly Leu Cys 245 250 255			768
50	aag cgc atg gac gct gac gcc gtg ccg acc cgg ggc gag acg att ggg Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly 260 265 270			816
55	aag aag acc gct tca agc gcc tgg gac ccg gca acc gtt atg cga atc Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile 275 280 285			864
60	ctt cgg gac ccg cgt att gcg ggc ttc gcc gct gag gtg atc tac aag Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys 290 295 300			912
65	aag aag ccg gac ggc acg ccg acc acg aag att gag ggt tac cgc att Lys Lys Pro Asp Gly Thr Pro Thr Thr Lys Ile Glu Gly Tyr Arg Ile 305 310 315 320			960
70	cag cgc gac ccg atc acg ctc ccg gtc gag ctt gat tgc gga ccg Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro 325 330 335			1008
75	atc atc gag ccc gct gag tgg tat gag ctt cag gcg tgg ttg gac ggc Ile Ile Glu Pro Ala Glu Trp Tyr Glu Leu Gln Ala Trp Leu Asp Gly 340 345 350			1056
80	agg ggg cgc ggc aag ggg ctt tcc ccg ggg caa gcc att ctg tcc gcc Arg Gly Arg Gly Lys Gly Leu Ser Arg Gly Gln Ala Ile Leu Ser Ala 355 360 365			1104
85	atg gac aag ctg tac tgc gag tgt ggc gcc gtc atg act tcg aag cgc			1152

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	385 390 395 400	
10	gtc gac ccc tcc gca cct ggg cag cac gaa ggc acg tgc aac gtc acg Val Asp Pro Ser Ala Pro Gly Gln His Glu Gly Thr Cys Asn Val Ser	1248
	405 410 415	
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	420 425 430	
20	agg cac gcc gaa ggc gac gaa gag acg ttg gcg ctt ctg tgg gaa gcc Arg His Ala Glu Gly Asp Glu Glu Thr Leu Ala Leu Leu Trp Glu Ala	1344
	435 440 445	
25	gcc cga cgc ttc ggc aag ctc act gag gcg cct gag aag agc ggc gaa Ala Arg Arg Phe Gly Lys Leu Thr Glu Ala Pro Glu Lys Ser Gly Glu	1392
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	465 470 475 480	
35	gag ctg tac gaa gac cgc gca ggc gcg tac gac gga ccc gtt ggc Glu Leu Tyr Glu Asp Arg Ala Ala Gly Ala Tyr Asp Gly Pro Val Gly	1488
	485 490 495	
40	agg aag cac ttc cgg aag caa cag gca gcg ctg acg ctc cgg cag caa Arg Lys His Phe Arg Lys Gln Gln Ala Ala Leu Thr Leu Arg Gln Gln	1536
	500 505 510	
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	515 520 525	
50	ctt ccc ctt gac caa tgg ttc ccc gaa gac gcc gac gct gac ccc acc Leu Pro Leu Asp Gln Trp Phe Pro Glu Asp Ala Asp Ala Asp Pro Thr	1632
	530 535 540	
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	565 570 575	
65	ggc agg ggg cag gga acg ccc atc gag aag cgc gct tcg atc acg tgg Gly Arg Gly Gln Gly Thr Pro Ile Glu Lys Arg Ala Ser Ile Thr Trp	1776
	580 585 590	
70	gcg aag ccg ccg acc gac gac gac gaa gac gac gcc cag gac ggc acg Ala Lys Pro Pro Thr Asp Asp Asp Glu Asp Asp Ala Gln Asp Gly Thr	1824
	595 600 605	
75	gaa gac gta gcg gcg cct aag aag aag agg aag gtt tag Glu Asp Val Ala Ala Pro Lys Lys Lys Arg Lys Val	1863
	610 615 620	
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<213> Artificial Sequence

<223> Description of Artificial Sequence: DNA sequence
coding for fusion protein C31-Int(CNLS)

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10 Asp Arg Gln Ser Arg Glu Arg Glu Asn Ser Ser Ala Ala Ser Pro Ala
 20 25 30

15 Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu
 35 40 45

20 Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu
 50 55 60

25 Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu
 65 70 75 80

30 Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val
 85 90 95

35 Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro
 100 105 110

40 Ile Val Ser Glu Leu Leu Ala Leu Gly Val Thr Ile Val Ser Thr Gln
 115 120 125

45 Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile
 130 135 140

50 Met Arg Leu Asp Ala Ser His Lys Glu Ser Ser Leu Lys Ser Ala Lys
 145 150 155 160

55 Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly
 165 170 175

60 Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile
 180 185 190

65 Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His
 195 200 205

70 Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile
 210 215 220

75 Arg Trp Trp Trp Arg Glu Ile Lys Thr His Lys His Leu Pro Phe Lys
 225 230 235 240

80 Pro Gly Ser Gln Ala Ala Ile His Pro Gly Ser Ile Thr Gly Leu Cys
 245 250 255

85 Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly
 260 265 270

90 Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile
 275 280 285

95 Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys
 290 295 300

100 Lys Lys Pro Asp Gly Thr Pro Thr Thr Lys Ile Glu Gly Tyr Arg Ile
 305 310 315 320

105 Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro
 325 330 335

Ile Ile Glu Pro Ala Glu Trp Tyr Glu Leu Gln Ala Trp Leu Asp Gly
 340 345 350

5 Arg Gly Arg Gly Lys Gly Leu Ser Arg Gly Gln Ala Ile Leu Ser Ala
 355 360 365

Met Asp Lys Leu Tyr Cys Glu Cys Gly Ala Val Met Thr Ser Lys Arg
 370 375 380

10 Gly Glu Glu Ser Ile Lys Asp Ser Tyr Arg Cys Arg Arg Arg Lys Val
 385 390 395 400

15 Val Asp Pro Ser Ala Pro Gly Gln His Glu Gly Thr Cys Asn Val Ser
 405 410 415

Met Ala Ala Leu Asp Lys Phe Val Ala Glu Arg Ile Phe Asn Lys Ile
 420 425 430

20 Arg His Ala Glu Gly Asp Glu Glu Thr Leu Ala Leu Leu Trp Glu Ala
 435 440 445

Ala Arg Arg Phe Gly Lys Leu Thr Glu Ala Pro Glu Lys Ser Gly Glu
 450 455 460

25 Arg Ala Asn Leu Val Ala Glu Arg Ala Asp Ala Leu Asn Ala Leu Glu
 465 470 475 480

30 Glu Leu Tyr Glu Asp Arg Ala Ala Gly Ala Tyr Asp Gly Pro Val Gly
 485 490 495

Arg Lys His Phe Arg Lys Gln Gln Ala Ala Leu Thr Leu Arg Gln Gln
 500 505 510

35 Gly Ala Glu Glu Arg Leu Ala Glu Leu Glu Ala Ala Glu Ala Pro Lys
 515 520 525

Leu Pro Leu Asp Gln Trp Phe Pro Glu Asp Ala Asp Ala Asp Pro Thr
 530 535 540

40 Gly Pro Lys Ser Trp Trp Gly Arg Ala Ser Val Asp Asp Lys Arg Val
 545 550 555 560

Phe Val Gly Leu Phe Val Asp Lys Ile Val Val Thr Lys Ser Thr Thr
 565 570 575

Gly Arg Gly Gln Gly Thr Pro Ile Glu Lys Arg Ala Ser Ile Thr Trp
 580 585 590

50 Ala Lys Pro Pro Thr Asp Asp Asp Glu Asp Asp Ala Gln Asp Gly Thr
 595 600 605

Glu Asp Val Ala Ala Pro Lys Lys Lys Arg Lys Val
 610 615 620

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 60 <212> PRT
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<220>
 65 <223> Description of Artificial Sequence: NLS

<400> 24
 Met Lys Lys Lys Lys Lys Lys Lys Lys Cys Arg Leu Lys

1 5 10 15

Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys
20 25 30

5 Lys Lys Lys Arg Arg Arg Lys Thr Lys Arg
35 40

10 <210> 25
<211> 10
<212> PRT
<213> Artificial Sequence

15 <220>
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<400> 25
0 Ile Lys Tyr Phe Lys Lys Phe Pro Lys Asp
1 5 10

5 <210> 26
<211> 14
<212> PRT
<213> Artificial Sequence

30 <220>
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<400> 26
35 Met Thr Gly Ser Lys Thr Arg Lys His Arg Gly Ser Gly Ala
1 5 10

40 <210> 27
<211> 14
<212> PRT
<213> Artificial Sequence

45 <220>
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<400> 27
45 Met Thr Gly Ser Lys His Arg Lys His Pro Gly Ser Gly Ala
1 5 10

50 <210> 28
<211> 7
<212> PRT
<213> Artificial Sequence

55 <220>
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<400> 28
Gly Lys Lys Arg Ser Lys Ala
1 5

60 <210> 29
<211> 14
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65 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: NLS
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1 5 10

<210> 30
<211> 11
10 <212> PRT
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<220>
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15 <400> 30
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1 5 10

<210> 31
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20 <213> Artificial Sequence

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25 <400> 31
Glu Glu Asp Gly Pro Gln Lys Lys Lys Arg Arg Leu
1 5 10

<210> 32
35 <211> 8
<212> PRT
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1 5

45 <210> 33
<211> 7
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50 <213> Artificial Sequence

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55 <400> 33
Pro Asn Lys Lys Lys Arg Lys
1 5

60 <210> 34
<211> 5
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65 <220>
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5 <400> 34
Lys Arg Pro Arg Pro
1 5

10 <210> 35
<211> 11
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15 <220>
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Cys Gly Gly Leu Ser Ser Lys Arg Pro Arg Pro
1 5 10

0 <210> 36
<211> 19
<212> PRT
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5 <220>
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0 <400> 36
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1 5 10 15

0 Lys Arg Pro

5 <210> 37
<211> 11
<212> PRT
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40 <220>
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45 <400> 37
Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys
1 5 10

50 <210> 38
<211> 9
<212> PRT
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55 <220>
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55 <400> 38
Pro Lys Gln Lys Arg Lys Met Ala Arg
1 5

60 <210> 39
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<212> PRT
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65 <220>
<223> Description of Artificial Sequence: NLS

5 <400> 39
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1 5
5
10 <210> 40
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<220>
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10 Cys Gly Gly Ala Ala Lys Arg Val Lys Leu Asp
1 5 10

20 <210> 41
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25 <220>
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20 Pro Ala Ala Lys Arg Val Lys Leu Asp
1 5

35 <210> 42
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40 <400> 42
35 Arg Gln Arg Arg Asn Glu Leu Lys Arg Ser Pro
1 5 10

45 <210> 43
<211> 8
<212> PRT
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50 <220>
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<400> 43
55 Pro Gln Ser Arg Lys Lys Leu Arg
1 5

60 <210> 44
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<220>
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<400> 44

Pro Leu Leu Lys Lys Ile Lys Gln
1 5

5 <210> 45
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15 1 5

0 <210> 46
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5 <220>
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<400> 46
Ser Lys Arg Val Ala Lys Arg Lys Leu
1 5

10 <210> 47
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<223> Description of Artificial Sequence: NLS

<400> 47
Ala Ser Lys Ser Arg Lys Arg Lys Leu
40 1 5

45 <210> 48
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50 <220>
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<400> 48
Gly Gly Leu Cys Ser Ala Arg Leu His Arg His Ala Leu Leu Ala Thr
1 5 10 15

55 <210> 49
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60 <220>
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65 <400> 49
Arg Lys Thr Lys Lys Lys Ile Lys
1 5

5 <210> 50
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10 <220>
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 Arg Lys Leu Lys Lys Leu Gly Asn
 1 5

15 <210> 51
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25 <400> 51
 Arg Lys Asp Arg Arg Gly Gly Arg
 1 5

30 <210> 52
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 <213> Artificial Sequence

35 <220>
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40 <400> 52
 Asp Thr Arg Glu Lys Lys Lys Phe Leu Lys Arg Arg Leu Leu Arg Leu
 1 5 10 15
 Asp Glu

45 <210> 53
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50 <220>
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55 <400> 53
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 1 5

60 <210> 54
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65 <220>
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 <400> 54

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10	tcg tgt cgc gag ctc tgc aag agc ctc ggc atg gag gtg ggg cag gtg Ser Cys Arg Glu Leu Cys Lys Ser Leu Gly Met Glu Val Gly Gln Val 35 40 45	144
15	tgg gtc gac aac gac ctg agc gcc acc aag aac gtc gtc cgc cct Trp Val Asp Asn Asp Leu Ser Ala Thr Lys Lys Asn Val Val Arg Pro 50 55 60	192
20	gac ttc gag gcg atg atc gcg agc aac ccg cag gcg atc gtc tgc tgg Asp Phe Glu Ala Met Ile Ala Ser Asn Pro Gln Ala Ile Val Cys Trp 65 70 75 80	240
25	cac acc gac cgg ctc atc cgc gtc acg ccg gac ctg gag cgg gtg atc His Thr Asp Arg Leu Ile Arg Val Thr Arg Asp Leu Glu Arg Val Ile 85 90 95	288
30	gac ctc gga gtc aac gtc cac gcc gtg atg gcc gga cac ctg gac ctg Asp Leu Gly Val Asn Val His Ala Val Met Ala Gly His Leu Asp Leu 100 105 110	336
35	tcc acc ccg gcc ggc cga gcc gtc gcc cgc acg gtg acg gcc tgg gcc Ser Thr Pro Ala Gly Arg Ala Val Ala Arg Thr Val Thr Ala Trp Ala 115 120 125	384
40	acg tac gag ggc gag cag aag gct gag cgc cag aag ctc gcc aac atc Thr Tyr Glu Gly Glu Gln Lys Ala Glu Arg Gln Lys Leu Ala Asn Ile 130 135 140	432
45	cag aac gcc cgc gcc ggc aag ccg tac acc ccc ggc atc cgc ccc ttc Gln Asn Ala Arg Ala Gly Lys Pro Tyr Thr Pro Gly Ile Arg Pro Phe 145 150 155 160	480
50	ggg tac ggc gac cac atg acc atc gtg acg gcc gag gcg gac gcc Gly Tyr Gly Asp Asp His Met Thr Ile Val Thr Ala Glu Ala Asp Ala 165 170 175	528
55	atc cgc gac ggc gcg aag atg atc ctc gac ggc tgg tcc ctg tcg gcc Ile Arg Asp Gly Ala Lys Met Ile Leu Asp Gly Trp Ser Leu Ser Ala 180 185 190	576
60	gtg gct cgc tac tgg gag gac ctc aag ctc cag tcg ccc cgg agt atg Val Ala Arg Tyr Trp Glu Glu Leu Lys Leu Gln Ser Pro Arg Ser Met 195 200 205	624
65	gcc gca ggc ggc aag ggc tgg tct ctg cgg ggc gta aag aag gtg ctg Ala Ala Gly Gly Lys Gly Trp Ser Leu Arg Gly Val Lys Lys Val Leu 210 215 220	672
70	acc tcc ccg cgc tac gtc ggg cgg tcc agc tac ctc ggg gag gtc gtg Thr Ser Pro Arg Tyr Val Gly Arg Ser Ser Tyr Leu Gly Glu Val Val 225 230 235 240	720
75	ggc gat gct cag tgg ccg ccc atc ctc gac ccg gac gtc tac tac ggg Gly Asp Ala Gln Trp Pro Pro Ile Leu Asp Pro Asp Val Tyr Tyr Gly 245 250 255	768
80	gtc gtg gcc atc ctg aac aac ccc gac cgc ttc agc ggg ggc cct cgg Val Val Ala Ile Leu Asn Asn Pro Asp Arg Phe Ser Gly Gly Pro Arg 260 265 270	816

	acc ggc cgc acc ccc ggc acg ctg ctc gca ggc atc gcc ttg tgc ggt	864
	Thr Gly Arg Thr Pro Gly Thr Leu Leu Ala Gly Ile Ala Leu Cys Gly	
5	275 280 285	
	gag tgc ggc aag acg gtc agt gga cgc ggc tac cga ggt gtc ctg gtc	912
	Glu Cys Gly Lys Thr Val Ser Gly Arg Gly Tyr Arg Gly Val Leu Val	
	290 295 300	
10	tac gga tgt aag gac acg cac act cgg acg cct cgg agc atc gct gac	960
	Tyr Gly Cys Lys Asp Thr His Thr Arg Thr Pro Arg Ser Ile Ala Asp	
	305 310 315 320	
15	ggc cgc gcg agc agc tcg acc ctc gcc cgg ctc atg ttc ccc gac ttc	1008
	Gly Arg Ala Ser Ser Ser Thr Leu Ala Arg Leu Met Phe Pro Asp Phe	
	325 330 335	
20	ctg ccc ggc ctc ctg gcc tct ggg cag gcc gag gac ggc cag tcg gca	1056
	Leu Pro Gly Leu Leu Ala Ser Gly Gln Ala Glu Asp Gly Gln Ser Ala	
	340 345 350	
25	gca tcc aag cac tcg gag gcc cag acg ctg cgc gag cgc ctt gac ggg	1104
	Ala Ser Lys His Ser Glu Ala Gln Thr Leu Arg Glu Arg Leu Asp Gly	
	355 360 365	
30	ctg gct acg gcc tac gcg gag ggt gcg atc acg ctg tct cag atg acg	1152
	Leu Ala Thr Ala Tyr Ala Glu Gly Ala Ile Ser Leu Ser Gln Met Thr	
	370 375 380	
35	gcc ggc tcg gaa gca ctg cgg aag aag ctg gag gtg atc gaa gcc gac	1200
	Ala Gly Ser Glu Ala Leu Arg Lys Leu Glu Val Ile Glu Ala Asp	
	385 390 395 400	
40	ctc gtg ggc tcg gca ggc atc ccg ccc ttc gat cca gtg gcc gga gtg	1248
	Leu Val Gly Ser Ala Gly Ile Pro Pro Phe Asp Pro Val Ala Gly Val	
	405 410 415	
45	gct ggc ctg atc tcc ggc tgg ccc acc acg cct ctc ccg acg cgt cga	1296
	Ala Gly Leu Ile Ser Gly Trp Pro Thr Thr Pro Leu Pro Thr Arg Arg	
	420 425 430	
50	gca tgg gtg gac ttc tgc ctg gtg gtc acg ctg aac acc cag aag ggg	1344
	Ala Trp Val Asp Phe Cys Leu Val Val Thr Leu Asn Thr Gln Lys Gly	
	435 440 445	
55	cgc cat gcg tcg agc atg acc gtg gac gac cac gtc acc atc gag tgg	1392
	Arg His Ala Ser Ser Met Thr Val Asp Asp His Val Thr Ile Glu Trp	
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	Arg Asp Val Ala Glu	
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	Ser Leu Asp Arg Thr Gly Glu Glu Leu Gly Val Glu Arg Gln Glu Glu	
	20 25 30	
	Ser Cys Arg Glu Leu Cys Lys Ser Leu Gly Met Glu Val Gly Gln Val	

35

40

45

Trp Val Asp Asn Asp Leu Ser Ala Thr Lys Lys Asn Val Val Arg Pro
 50 55 60

Asp Phe Glu Ala Met Ile Ala Ser Asn Pro Gln Ala Ile Val Cys Trp
 65 70 75 80

His Thr Asp Arg Leu Ile Arg Val Thr Arg Asp Leu Glu Arg Val Ile
 10 85 90 95

Asp Leu Gly Val Asn Val His Ala Val Met Ala Gly His Leu Asp Leu
 100 105 110

Ser Thr Pro Ala Gly Arg Ala Val Ala Arg Thr Val Thr Ala Trp Ala
 15 115 120 125

Thr Tyr Glu Gly Glu Gln Lys Ala Glu Arg Gln Lys Leu Ala Asn Ile
 130 135 140

Gln Asn Ala Arg Ala Gly Lys Pro Tyr Thr Pro Gly Ile Arg Pro Phe
 145 150 155 160

Gly Tyr Gly Asp Asp His Met Thr Ile Val Thr Ala Glu Ala Asp Ala
 165 170 175

Ile Arg Asp Gly Ala Lys Met Ile Leu Asp Gly Trp Ser Leu Ser Ala
 180 185 190

Val Ala Arg Tyr Trp Glu Glu Leu Lys Leu Gln Ser Pro Arg Ser Met
 30 195 200 205

Ala Ala Gly Gly Lys Gly Trp Ser Leu Arg Gly Val Lys Lys Val Leu
 210 215 220

Thr Ser Pro Arg Tyr Val Gly Arg Ser Ser Tyr Leu Gly Glu Val Val
 225 230 235 240

Gly Asp Ala Gln Trp Pro Pro Ile Leu Asp Pro Asp Val Tyr Tyr Gly
 40 245 250 255

Val Val Ala Ile Leu Asn Asn Pro Asp Arg Phe Ser Gly Gly Pro Arg
 260 265 270

45 Thr Gly Arg Thr Pro Gly Thr Leu Leu Ala Gly Ile Ala Leu Cys Gly
 275 280 285

Glu Cys Gly Lys Thr Val Ser Gly Arg Gly Tyr Arg Gly Val Leu Val
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Tyr Gly Cys Lys Asp Thr His Thr Arg Thr Pro Arg Ser Ile Ala Asp
 50 305 310 315 320

Gly Arg Ala Ser Ser Ser Thr Leu Ala Arg Leu Met Phe Pro Asp Phe
 55 325 330 335

Leu Pro Gly Leu Leu Ala Ser Gly Gln Ala Glu Asp Gly Gln Ser Ala
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60 Ala Ser Lys His Ser Glu Ala Gln Thr Leu Arg Glu Arg Leu Asp Gly
 355 360 365

Leu Ala Thr Ala Tyr Ala Glu Gly Ala Ile Ser Leu Ser Gln Met Thr
 370 375 380

65 Ala Gly Ser Glu Ala Leu Arg Lys Lys Leu Glu Val Ile Glu Ala Asp
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Leu Val Gly Ser Ala Gly Ile Pro Pro Phe Asp Pro Val Ala Gly Val
 405 410

5 Ala Gly Leu Ile Ser Gly Trp Pro Thr Thr Pro Leu Pro Thr Arg Arg
 420 425 430

Ala Trp Val Asp Phe Cys Leu Val Val Thr Leu Asn Thr Gln Lys Gly
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10 Arg His Ala Ser Ser Met Thr Val Asp Asp His Val Thr Ile Glu Trp
 450 455 460

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 Gly Ser Ser Ile Asp Ser Gln Ile Glu Ala Cys Ile Lys Lys Ala Gly
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 Thr Lys Asp Val Leu Lys Tyr Ala Asp Glu Gly Phe Ser Gly Glu Leu
 35 40 45

tta gaa cgt ccg gct ttg aat cgc ttg agg gag gat gca agc aag gga 192
 Leu Glu Arg Pro Ala Leu Asn Arg Leu Arg Glu Asp Ala Ser Lys Gly
 50 55 60

45 ctt ata agt caa gtc att tgt tac gat cct gac cgt ctt tct cgg aaa 240
 Leu Ile Ser Gln Val Ile Cys Tyr Asp Pro Asp Arg Leu Ser Arg Lys
 65 70 75 80

50 tta atg aat cag cta atc att gat gac gaa ttg cga aag cga aac ata 288
 Leu Met Asn Gln Leu Ile Ile Asp Asp Glu Leu Arg Lys Arg Asn Ile
 85 90 95

55 cct ttg att ttt gta aat ggt gaa tac gcc aat tct cca gaa ggt caa 336
 Pro Leu Ile Phe Val Asn Gly Glu Tyr Ala Asn Ser Pro Glu Gly Gln
 100 105 110

60 ttg ttt ttc gca atg cgc ggg gca atc tca gaa ttt gaa aaa gcc aaa 384
 Leu Phe Ala Met Arg Gly Ala Ile Ser Glu Phe Glu Lys Ala Lys
 115 120 125

65 atc aaa gaa cgg aca tca agc ggc cga ctt caa aaa atg aaa aaa ggc 432
 Ile Lys Glu Arg Thr Ser Ser Gly Arg Leu Gln Lys Met Lys Lys Gly
 130 135 140

atg atc att aaa gat tct aaa cta tat ggc tat aaa ttt gtt aaa gag 480
 Met Ile Ile Lys Asp Ser Lys Leu Tyr Gly Tyr Lys Phe Val Lys Glu
 145 150 155 160

	aaa aga act ctt gag ata tta gaa gag gaa gca aaa atc att cgg atg Lys Arg Thr Leu Glu Ile Leu Glu Glu Ala Lys Ile Ile Arg Met 165 170 175	528
5	att ttt aac tat ttc acc gat cat aaa agc cct ttt ttc ggc aga gta Ile Phe Asn Tyr Phe Thr Asp His Lys Ser Pro Phe Phe Gly Arg Val 180 185 190	576
10	aat ggt att gct cta cat tta act cag atg ggg gtt aaa aca aaa aaa Asn Gly Ile Ala Leu His Leu Thr Gln Met Gly Val Lys Thr Lys Lys 195 200 205	624
15	ggc gcc aaa gta tgg cac agg cag gtt gtt cgg caa ata tta atg aac Gly Ala Lys Val Trp His Arg Gln Val Val Arg Gln Ile Leu Met Asn 210 215 220	672
20	tct tcc tat aag ggt gaa cat aga cag tat aaa tat gat aca gag ggt Ser Ser Tyr Lys Gly His Arg Gln Tyr Lys Tyr Asp Thr Glu Gly 225 230 235 240	720
25	tcc tat gtt tca aag cag gca ggg aac aaa tct ata att aaa ata agg Ser Tyr Val Ser Lys Gln Ala Gly Asn Lys Ser Ile Ile Lys Ile Arg 245 250 255	768
30	cct gaa gaa gaa caa atc act gtg aca att cca gca att gtt cca gct Pro Glu Glu Glu Gln Ile Thr Val Thr Ile Pro Ala Ile Val Pro Ala 260 265 270	816
35	gaa caa tgg gat tat gct caa gaa ctc tta ggt caa agt aaa aga aaa Glu Gln Trp Asp Tyr Ala Gln Glu Leu Leu Gly Gln Ser Lys Arg Lys 275 280 285	864
40	cac ttg agt atc agc cct cac aat tac ttg tta tcg ggt ttg gtt aga His Leu Ser Ile Ser Pro His Asn Tyr Leu Leu Ser Gly Leu Val Arg 290 295 300	912
45	tgc gga aaa tgc gga aat acc atg aca ggg aag aaa aga aaa tca cat Cys Gly Lys Cys Gly Asn Thr Met Thr Gly Lys Lys Arg Lys Ser His 305 310 315 320	960
50	gtt aaa gac tac tat gta tat act tgc cgg aaa aat tat tct ggc gca Gly Lys Asp Tyr Tyr Val Tyr Thr Cys Arg Lys Asn Tyr Ser Gly Ala 325 330 335	1008
55	aag gac cgc ggc tgc gga aaa gaa atg tct gag aat aaa ttg aac cgg Lys Asp Arg Gly Cys Gly Lys Glu Met Ser Glu Asn Lys Leu Asn Arg 340 345 350	1056
60	cat gta tgg ggt gaa att ttt aaa ttc atc aca aat cct caa aag tat His Val Trp Gly Glu Ile Phe Lys Phe Ile Thr Asn Pro Gln Lys Tyr 355 360 365	1104
65	gtt tct ttt aaa gag gct gaa caa tca aat cac ctg tct gat gaa tta Val Ser Phe Lys Glu Ala Glu Gln Ser Asn His Leu Ser Asp Glu Leu 370 375 380	1152
70	gaa ctt att gaa aaa gag ata gag aaa aca aaa aaa ggc cgc aag cgt Glu Leu Ile Glu Lys Glu Ile Glu Lys Thr Lys Lys Gly Arg Lys Arg 385 390 395 400	1200
75	ctt tta acg cta atc agc cta agc gat gac gat gat tta gac ata gat Leu Leu Thr Leu Ile Ser Leu Ser Asp Asp Asp Asp Leu Asp Ile Asp 405 410 415	1248
80	gaa atc aaa gca caa att att gaa ctg caa aaa aag caa aat cag ctt Glu Ile Lys Ala Gln Ile Ile Glu Leu Gln Lys Lys Gln Asn Gln Leu	1296

420

425

430

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	acg agc tca agt gaa aat gct cta aaa aga gcc atc gac tat ttt caa		1392	
	Thr Ser Ser Glu Asn Ala Leu Lys Arg Ala Ile Asp Tyr Phe Gln			
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10	tca atc ggt gca gat aac tta act ctt gaa gat aaa aaa aca att gtt		1440	
	Ser Ile Gly Ala Asp Asn Leu Thr Leu Glu Asp Lys Lys Thr Ile Val			
	465	470	475	480
15	aac ttt atc gtg aaa gaa gtt acc att gtg gat tct gac acc ata tat		1488	
	Asn Phe Ile Val Lys Glu Val Thr Ile Val Asp Ser Asp Thr Ile Tyr			
	485	490	495	
20	att gaa acg tat taa		1503	
	Ile Glu Thr Tyr			
	500			
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	<211> 500			
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	<213> CisA recombinase			
30	<400> 57			
	Val Ile Ala Ile Tyr Val Arg Val Ser Thr Glu Glu Gln Ala Ile Lys			
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	Gly Ser Ser Ile Asp Ser Gln Ile Glu Ala Cys Ile Lys Lys Ala Gly			
	20	25	30	
35	Thr Lys Asp Val Leu Lys Tyr Ala Asp Glu Gly Phe Ser Gly Glu Leu			
	35	40	45	
40	Leu Glu Arg Pro Ala Leu Asn Arg Leu Arg Glu Asp Ala Ser Lys Gly			
	50	55	60	
	Leu Ile Ser Gln Val Ile Cys Tyr Asp Pro Asp Arg Leu Ser Arg Lys			
	65	70	75	80
45	Leu Met Asn Gln Leu Ile Ile Asp Asp Glu Leu Arg Lys Arg Asn Ile			
	85	90	95	
	Pro Leu Ile Phe Val Asn Gly Glu Tyr Ala Asn Ser Pro Glu Gly Gln			
50	100	105	110	
	Leu Phe Phe Ala Met Arg Gly Ala Ile Ser Glu Phe Glu Lys Ala Lys			
	115	120	125	
55	Ile Lys Glu Arg Thr Ser Ser Gly Arg Leu Gln Lys Met Lys Lys Gly			
	130	135	140	
	Met Ile Ile Lys Asp Ser Lys Leu Tyr Gly Tyr Lys Phe Val Lys Glu			
	145	150	155	160
60	Lys Arg Thr Leu Glu Ile Leu Glu Glu Ala Lys Ile Ile Arg Met			
	165	170	175	
	Ile Phe Asn Tyr Phe Thr Asp His Lys Ser Pro Phe Phe Gly Arg Val			
65	180	185	190	
	Asn Gly Ile Ala Leu His Leu Thr Gln Met Gly Val Lys Thr Lys Lys			
	195	200	205	

Gly Ala Lys Val Trp His Arg Gln Val Val Arg Gln Ile Leu Met Asn
 210 215 220

5 Ser Ser Tyr Lys Gly Glu His Arg Gln Tyr Lys Tyr Asp Thr Glu Gly
 225 230 235 240

Ser Tyr Val Ser Lys Gln Ala Gly Asn Lys Ser Ile Ile Lys Ile Arg
 245 250 255

10 Pro Glu Glu Glu Gln Ile Thr Val Thr Ile Pro Ala Ile Val Pro Ala
 260 265 270

15 Glu Gln Trp Asp Tyr Ala Gln Glu Leu Leu Gly Gln Ser Lys Arg Lys
 275 280 285

His Leu Ser Ile Ser Pro His Asn Tyr Leu Leu Ser Gly Leu Val Arg
 290 295 300

20 Cys Gly Lys Cys Gly Asn Thr Met Thr Gly Lys Lys Arg Lys Ser His
 305 310 315 320

Gly Lys Asp Tyr Tyr Val Tyr Thr Cys Arg Lys Asn Tyr Ser Gly Ala
 325 330 335

25 Lys Asp Arg Gly Cys Gly Lys Glu Met Ser Glu Asn Lys Leu Asn Arg
 340 345 350

30 His Val Trp Gly Glu Ile Phe Lys Phe Ile Thr Asn Pro Gln Lys Tyr
 355 360 365

Val Ser Phe Lys Glu Ala Glu Gln Ser Asn His Leu Ser Asp Glu Leu
 370 375 380

35 Glu Leu Ile Glu Lys Glu Ile Glu Lys Thr Lys Lys Gly Arg Lys Arg
 385 390 395 400

Leu Leu Thr Leu Ile Ser Leu Ser Asp Asp Asp Asp Leu Asp Ile Asp
 405 410 415

40 Glu Ile Lys Ala Gln Ile Ile Glu Leu Gln Lys Lys Gln Asn Gln Leu
 420 425 430

Thr Glu Lys Cys Asn Arg Ile Gln Ser Lys Met Lys Val Leu Asp Asp
 435 440 445

Thr Ser Ser Ser Glu Asn Ala Leu Lys Arg Ala Ile Asp Tyr Phe Gln
 450 455 460

45 Ser Ile Gly Ala Asp Asn Leu Thr Leu Glu Asp Lys Lys Thr Ile Val
 465 470 475 480

Asn Phe Ile Val Lys Glu Val Thr Ile Val Asp Ser Asp Thr Ile Tyr
 485 490 495

50 Ile Glu Thr Tyr
 55 500

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10 gat aaa ggt gcg ttg cgt aaa caa ata gaa cgc ttg cgt aat gct gga Asp Lys Gly Ala Leu Arg Lys Gln Ile Glu Arg Leu Arg Asn Ala Gly 20 25 30	96
15 tgt tca aaa gtg tac tgg gat att caa tcg cgg aca.act gaa gtc aga Cys Ser Lys Val Tyr Trp Asp Ile Gln Ser Arg Thr Thr Glu Val Arg 35 40 45	144
20 gaa ggg cta caa caa tta att aat gac tta aag aca tct tca aca ggt Glu Gly Leu Gln Gln Leu Ile Asn Asp Leu Lys Thr Ser Ser Thr Gly 50 55 60	192
25 aag gta aaa tca ctg caa ttt acc cgc att gat cgc atc ggc tca tca Lys Val Lys Ser Ile Gln Phe Thr Arg Ile Asp Arg Ile Gly Ser Ser 65 70 75 80	240
30 tcg cgg ttg ttt tat tca ttg tta gag gta tta cgt tcc aag gga att Ser Arg Leu Phe Tyr Ser Ile Leu Glu Val Leu Arg Ser Lys Gly Ile 85 90 95	288
35 aaa ctg ata gcc tta gat caa ggc gtt gac cca gac agc ctt ggc ggg Lys Leu Ile Ala Leu Asp Gln Gly Val Asp Pro Asp Ser Leu Gly Gly 100 105 110	336
40 gaa cta aca att gat atg tta ctg gct gct gcc aaa ttt gag gta aga Glu Leu Thr Ile Asp Met Leu Ala Ala Ala Lys Phe Glu Val Arg 115 120 125	384
45 atg gtg acg gag agg tta aaa agc gaa cgt cgt cat agg gtg aac caa Met Val Thr Glu Arg Leu Lys Ser Glu Arg Arg His Arg Val Asn Gln 130 135 140	432
50 gga aaa agt cac cga gtt gcc cca tta gga tac cgc aaa gat aaa gat Gly Lys Ser His Arg Val Ala Pro Leu Gly Tyr Arg Lys Asp Lys Asp 145 150 155 160	480
55 aaa tat ata cgc gat cgc tca cca tgt gtt tgc tta cta gaa gga cgc Lys Tyr Ile Arg Asp Arg Ser Pro Cys Val Cys Leu Leu Glu Gly Arg 165 170 175	528
60 aga gaa tta acg gtg tct gac tta gcc cag tat att ttt cac act ttt Arg Glu Leu Thr Val Ser Asp Leu Ala Gln Tyr Ile Phe His Thr Phe 180 185 190	576
65 ttt gag tgc ggt tcc gtt gct gct act gtg cgt aag ctg cac tca gat Phe Glu Cys Gly Ser Val Ala Ala Thr Val Arg Lys Leu His Ser Asp 195 200 205	624
70 ttt ggt ata gaa aca aaa gtt ctg aat tgg aac aag cta gaa aaa tct Phe Gly Ile Glu Thr Lys Val Leu Asn Trp Asn Lys Leu Glu Lys Ser 210 215 220	672
75 tcc cgg att gtt ggc gac gac gac tta gat aaa att gca ttt aca cca Ser Arg Ile Val Gly Asp Asp Leu Asp Lys Ile Ala Phe Thr Pro 225 230 235 240	720
80 aat aaa act aac cac ccc ttg cgt tat ccc tgg tct ggg cta aga tgg Asn Lys Thr Asn His Pro Leu Arg Tyr Pro Trp Ser Gly Leu Arg Trp 245 250 255	768

	tca atc cct ggt tta aaa gcg tta tta gtt aac cct gtt tac gcc ggg Ser Ile Pro Gly Leu Lys Ala Leu Leu Val Asn Pro Val Tyr Ala Gly 260 265 270	816
5	ggt ttg ccc ttt gat act tac gtt aaa tca aaa gga aaa cgc aag cat Gly Leu Pro Phe Asp Thr Tyr Val Lys Ser Lys Gly Lys Arg Lys His 275 280 285	864
10	ttt gac gag tgg aaa gta aaa tgg gga acc cac gac gat gag gca atc Phe Asp Glu Trp Lys Val Lys Trp Gly Thr His Asp Asp Glu Ala Ile 290 295 300	912
15	att acc tgt gag gaa cat gaa aga ata aaa cag atg att cga gac aat Ile Thr Cys Glu Glu His Glu Arg Ile Lys Gln Met Ile Arg Asp Asn 305 310 315 320	960
20	cgc aat aat cga tgg gct gca aga gaa gaa aac gaa gta aac cca ttt Arg Asn Asn Arg Trp Ala Ala Arg Glu Asn Glu Val Asn Pro Phe 325 330 335	1008
25	tct aat tta ctt aaa tgt acc cat tgc ggc ggc tca atg aca cgc cac Ser Asn Leu Leu Lys Cys Thr His Cys Gly Ser Met Thr Arg His 340 345 350	1056
30	gcc aaa cgt gta gat aag agt gga caa gct atc tat tat tat cag tgc Ala Lys Arg Val Asp Lys Ser Gly Gln Ala Ile Tyr Tyr Gln Cys 355 360 365	1104
35	cga ttg tat aaa gct ggc aac tgt agc aat aaa aat atg att tca tcc Arg Leu Tyr Lys Ala Gly Asn Cys Ser Asn Lys Asn Met Ile Ser Ser 370 375 380	1152
40	aaa ata tta gat atc caa gta atg gat tta ttg gca caa gaa gcc gaa Lys Ile Leu Asp Ile Gln Val Met Asp Leu Leu Ala Gln Glu Ala Glu 385 390 395 400	1200
45	cgt tta gca aat ttg gtg gaa aca gat gag ccg ctt att gta gaa gaa Arg Leu Ala Asn Leu Val Glu Thr Asp Glu Pro Leu Ile Val Glu Glu 405 410 415	1248
50	ccc cca gaa gta aaa acg ctg cgc gca tcc ctg aat agt ctg gaa aca Pro Pro Glu Val Lys Thr Leu Arg Ala Ser Leu Asn Ser Leu Glu Thr 420 425 430	1296
55	ttg cca gca agt tca gca att gaa caa att aaa aat gac ctc aaa gaa Leu Pro Ala Ser Ser Ala Ile Glu Gln Ile Lys Asn Asp Leu Lys Glu 435 440 445	1344
60	cag att ggc atc gca cta gga gca acc aat aat gct tct aaa caa tct Gln Ile Ala Ile Ala Leu Gly Ala Thr Asn Asn Ala Ser Lys Gln Ser 450 455 460	1392
65	ctg att gcc aag gaa aga att ata caa gct ttt gct cat aaa agt tac Leu Ile Ala Lys Glu Arg Ile Ile Gln Ala Phe Ala His Lys Ser Tyr 465 470 475 480	1440
70	tgg caa gga cta aac gct caa gat aaa cga gca atc ctc aat ggt tgc Trp Gln Gly Leu Asn Ala Gln Asp Lys Arg Ala Ile Leu Asn Gly Cys 485 490 495	1488
75	gta aaa aaa atc tcc gta gat ggt aac ttt gtt aca gct att gag tat Val Lys Lys Ile Ser Val Asp Gly Asn Phe Val Thr Ala Ile Glu Tyr 500 505 510	1536
80	cgt tac tag Arg Tyr	1545

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 10 Asp Lys Gly Ala Leu Arg Lys Gln Ile Glu Arg Leu Arg Asn Ala Gly
 20 25 30
 15 Cys Ser Lys Val Tyr Trp Asp Ile Gln Ser Arg Thr Thr Glu Val Arg
 35 40 45
 20 Glu Gly Leu Gln Gln Leu Ile Asn Asp Leu Lys Thr Ser Ser Thr Gly
 50 55 60
 25 Lys Val Lys Ser Leu Gln Phe Thr Arg Ile Asp Arg Ile Gly Ser Ser
 65 70 75 80
 30 Ser Arg Leu Phe Tyr Ser Leu Leu Glu Val Leu Arg Ser Lys Gly Ile
 85 90 95
 35 Lys Leu Ile Ala Leu Asp Gln Gly Val Asp Pro Asp Ser Leu Gly Gly
 100 105 110
 40 Glu Leu Thr Ile Asp Met Leu Leu Ala Ala Ala Lys Phe Glu Val Arg
 115 120 125
 45 Met Val Thr Glu Arg Leu Lys Ser Glu Arg Arg His Arg Val Asn Gln
 130 135 140
 50 Gly Lys Ser His Arg Val Ala Pro Leu Gly Tyr Arg Lys Asp Lys Asp
 145 150 155 160
 55 Lys Tyr Ile Arg Asp Arg Ser Pro Cys Val Cys Leu Leu Glu Gly Arg
 165 170 175
 60 Arg Glu Leu Thr Val Ser Asp Leu Ala Gln Tyr Ile Phe His Thr Phe
 180 185 190
 65 Phe Glu Cys Gly Ser Val Ala Ala Thr Val Arg Lys Leu His Ser Asp
 195 200 205
 70 Phe Gly Ile Glu Thr Lys Val Leu Asn Trp Asn Lys Leu Glu Lys Ser
 210 215 220
 75 Ser Arg Ile Val Gly Asp Asp Asp Leu Asp Lys Ile Ala Phe Thr Pro
 225 230 235 240
 80 Asn Lys Thr Asn His Pro Leu Arg Tyr Pro Trp Ser Gly Leu Arg Trp
 245 250 255
 85 Ser Ile Pro Gly Leu Lys Ala Leu Leu Val Asn Pro Val Tyr Ala Gly
 260 265 270
 90 Gly Leu Pro Phe Asp Thr Tyr Val Lys Ser Lys Gly Lys Arg Lys His
 275 280 285
 95 Phe Asp Glu Trp Lys Val Lys Trp Gly Thr His Asp Asp Glu Ala Ile
 290 295 300
 100 Ile Thr Cys Glu Glu His Glu Arg Ile Lys Gln Met Ile Arg Asp Asn
 305 310 315 320

Arg Asn Asn Arg Trp Ala Ala Arg Glu Glu Asn Glu Val Asn Pro Phe
 325 330 335

5 Ser Asn Leu Leu Lys Cys Thr His Cys Gly Gly Ser Met Thr Arg His
 340 345 350

Ala Lys Arg Val Asp Lys Ser Gly Gln Ala Ile Tyr Tyr Gln Cys
 355 360 365

10 Arg Leu Tyr Lys Ala Gly Asn Cys Ser Asn Lys Asn Met Ile Ser Ser
 370 375 380

Lys Ile Leu Asp Ile Gln Val Met Asp Leu Leu Ala Gln Glu Ala Glu
 385 390 395 400

15 Arg Leu Ala Asn Leu Val Glu Thr Asp Glu Pro Leu Ile Val Glu Glu
 405 410 415

0 Pro Pro Glu Val Lys Thr Leu Arg Ala Ser Leu Asn Ser Leu Glu Thr
 420 425 430

Leu Pro Ala Ser Ser Ala Ile Glu Gln Ile Lys Asn Asp Leu Lys Glu
 435 440 445

15 Gln Ile Ala Ile Ala Leu Gly Ala Thr Asn Asn Ala Ser Lys Gln Ser
 450 455 460

Leu Ile Ala Lys Glu Arg Ile Ile Gln Ala Phe Ala His Lys Ser Tyr
 465 470 475 480

30 Trp Gln Gly Leu Asn Ala Gln Asp Lys Arg Ala Ile Leu Asn Gly Cys
 485 490 495

35 Val Lys Lys Ile Ser Val Asp Gly Asn Phe Val Thr Ala Ile Glu Tyr
 500 505 510

Arg Tyr

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 45 <213> Transposon Tn4451

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55 gat gat gac ctt act ggc gag agt aat tct att acc aat caa aag aaa 96
 Asp Asp Asp Leu Thr Gly Glu Ser Asn Ser Ile Thr Asn Gln Lys Lys
 20 25 30

60 tac ctc gaa gat tat gcc cgt agg aat ggt ttt gag aac att cgc cat 144
 Tyr Leu Glu Asp Tyr Ala Arg Arg Asn Gly Phe Glu Asn Ile Arg His
 35 40 45

65 ttt acc gat gac gga ttt tcg ggt gta aat ttc aat cgc cct ggc ttt 192
 Phe Thr Asp Asp Gly Phe Ser Gly Val Asn Phe Asn Arg Pro Gly Phe
 50 55 60

	caa tct ctg ata aaa gaa gtt gaa gca gga aat gta gaa acc ttg att	240
	Gln Ser Leu Ile Lys Glu Val Glu Ala Gly Asn Val Glu Thr Leu Ile	
	65 70 75 80	
5	gtt aag gat atg agc cga ttg ggg cga aat tat ctg caa gta ggt ttt	288
	Val Lys Asp Met Ser Arg Leu Gly Arg Asn Tyr Leu Gln Val Gly Phe	
	85 90 95	
10	tat acg gaa gtt ctg ttt cca cag aaa aat gtc cgt ttc ctt gca att	336
	Tyr Thr Glu Val Leu Phe Pro Gln Lys Asn Val Arg Phe Leu Ala Ile	
	100 105 110	
15	aac aac agt att gac agt aac aac gct tcg gat aat gac ttt gct ccg	384
	Asn Asn Ser Ile Asp Ser Asn Asn Ala Ser Asp Asn Asp Phe Ala Pro	
	115 120 125	
	ttt ttg aat att atg aac gaa tgg tat gcc aaa gac aca agc aac aaa	432
	Phe Leu Asn Ile Met Asn Glu Trp Tyr Ala Lys Asp Thr Ser Asn Lys	
	130 135 140	
20	atc aag gct ata ttc gat gcc cgt atg aaa gac gga aag cgt tgt agc	480
	Ile Lys Ala Ile Phe Asp Ala Arg Met Lys Asp Gly Lys Arg Cys Ser	
	145 150 155 160	
25	ggt tct atc cct tat ggg tat aac cga ctg ccg agc gac aaa caa acc	528
	Gly Ser Ile Pro Tyr Gly Tyr Asn Arg Leu Pro Ser Asp Lys Gln Thr	
	165 170 175	
30	ctt gtg gtt gac cct gtg gct tcg gaa gtg gta aag cgt atc ttt act	576
	Leu Val Val Asp Pro Val Ala Ser Glu Val Val Lys Arg Ile Phe Thr	
	180 185 190	
35	ctt gcc aat gat ggc aaa agt aca agg gca atc gca gaa ata ctg acc	624
	Leu Ala Asn Asp Gly Lys Ser Thr Arg Ala Ile Ala Glu Ile Leu Thr	
	195 200 205	
	gaa gaa aaa gtt tta acc cct gcg gca tac gca aag gaa tac cac ccc	672
	Glu Glu Lys Val Leu Thr Pro Ala Ala Tyr Ala Lys Glu Tyr His Pro	
	210 215 220	
40	gaa cag tac aac ggc aac aag ttc aca aac cct tat ctt tgg gca atg	720
	Glu Gln Tyr Asn Gly Asn Lys Phe Thr Asn Pro Tyr Leu Trp Ala Met	
	225 230 235 240	
45	tca acg ata aga aat att tta ggc agg cag gaa tat ctc ggt cac acc	768
	Ser Thr Ile Arg Asn Ile Leu Gly Arg Gln Glu Tyr Leu Gly His Thr	
	245 250 255	
50	gtt ttg cga aag tcg gta agc aca aat ttc aaa ctt cac aag aga aaa	816
	Val Leu Arg Lys Ser Val Ser Thr Asn Phe Lys Leu His Lys Arg Lys	
	260 265 270	
55	agc aca gac gaa gaa gag tat gta ttt ccg aat aca cac gag cct	864
	Ser Thr Asp Glu Glu Gln Tyr Val Phe Pro Asn Thr His Glu Pro	
	275 280 285	
60	atc ata tcg cag gaa ctt tgg gac agc gtt caa aaa cgc aga agc aga	912
	Ile Ile Ser Gln Glu Leu Trp Asp Ser Val Gln Lys Arg Arg Ser Arg	
	290 295 300	
	gta aat cgt gcc tcg gct tgg gga acg cac agc aac cgt tta agc gga	960
	Val Asn Arg Ala Ser Ala Trp Gly Thr His Ser Asn Arg Leu Ser Gly	
	305 310 315 320	
65	tat ttg tac tgt gcc gat tgc gga aga aga atg act ttg cag aca cat	1008
	Tyr Leu Tyr Cys Ala Asp Cys Gly Arg Arg Met Thr Leu Gln Thr His	
	325 330 335	

	tac agc aaa aaa gac ggt tct gtg cag tat tct tac cgt tgc ggt ggg Tyr Ser Lys Lys Asp Gly Ser Val Gln Tyr Ser Tyr Arg Cys Gly Gly 340 345 350	1056
5	tat gca agc aga gtg aac agt tgt acc agt cat tcg att agt acc gat Tyr Ala Ser Arg Val Asn Ser Cys Thr Ser His Ser Ile Ser Thr Asp 355 360 365	1104
10	aat gtt gaa gcc ttg ata tta tca tct gtc aaa cgc ttt tca agg ttt Asn Val Glu Ala Leu Ile Leu Ser Ser Val Lys Arg Phe Ser Arg Phe 370 375 380	1152
15	gtt ctg aat gat gaa caa gca ttt gct ttg gaa ctg caa tct ctt tgg Val Leu Asn Asp Glu Gln Ala Phe Ala Leu Glu Leu Gln Ser Leu Trp 385 390 395 400	1200
20	aat gaa aaa cag gag gaa aag ccg aaa cac aat caa tcg gaa ctg caa Asn Glu Lys Gln Glu Lys Pro Lys His Asn Gln Ser Glu Leu Gln 405 410 415	1248
25	cgc tgt cag aaa cgc tat gac gaa ctc tct acc ctt gtt cgt ggc ttg Arg Cys Gln Lys Arg Tyr Asp Glu Leu Ser Thr Leu Val Arg Gly Leu 420 425 430	1296
30	tat gaa aat ctt atg tcg gga tta ctg ccc gaa aga cag tat aag caa Tyr Glu Asn Leu Met Ser Gly Leu Leu Pro Glu Arg Gln Tyr Lys Gln 435 440 445	1344
35	ctg atg aaa cag tat gat gac gag cag gca gag ttg gaa acg aaa atg Leu Met Lys Gln Tyr Asp Asp Glu Gln Ala Glu Leu Glu Thr Lys Met 450 455 460	1392
40	gaa acg atg aaa aca gaa ctt gcc gaa gaa aaa gta agt tcc gtt gat Glu Thr Met Lys Thr Glu Leu Ala Glu Glu Lys Val Ser Ser Val Asp 465 470 475 480	1440
45	att aag cat ttc att tcg ctg ata cgc aag tgt aaa aat cct acg gaa Ile Lys His Phe Ile Ser Leu Ile Arg Lys Cys Lys Asn Pro Thr Glu 485 490 495	1488
50	atc tcc gat aca atg ttt aat gaa ctt gtt gat aag ata gtg gtt tat Ile Ser Asp Thr Met Phe Asn Glu Leu Val Asp Lys Ile Val Val Tyr 500 505 510	1536
55	gaa gca gag ggt gtg gga aaa gca cga aca caa aag gtc gat att tat Glu Ala Glu Gly Val Gly Lys Ala Arg Thr Gln Lys Val Asp Ile Tyr 515 520 525	1584
60	ttt aac tat gtc ggt caa gtg gat att gcc tat acc gaa gaa gaa ctt Phe Asn Tyr Val Gly Gln Val Asp Ile Ala Tyr Thr Glu Glu Glu Leu 530 535 540	1632
65	gcc gag ata gaa aca cag aaa gag cag gag gaa cag caa cgc ttg gca Ala Glu Ile Glu Thr Gln Lys Glu Gln Glu Glu Gln Gln Arg Leu Ala 545 550 555 560	1680
	aga cag cgc aag cgt gaa aaa gcc tac cga gaa aag cga aag gca cag Arg Gln Arg Lys Arg Glu Lys Ala Tyr Arg Glu Lys Arg Lys Ala Gln 565 570 575	1728
	aaa atc gct gaa aac ggt ggc gaa atc gtt aag aca aag gtt tgc cct Lys Ile Ala Glu Asn Gly Gly Glu Ile Val Lys Thr Lys Val Cys Pro 580 585 590	1776
	cat tgc aac aaa gag ttt atc ccg aca agc aac cga cag gtg ttc tgt His Cys Asn Lys Glu Phe Ile Pro Thr Ser Asn Arg Gln Val Phe Cys	1824

	595	600	605	
5	tcc aaa gag tgc tgc tat caa gca agg caa gac aaa aag aaa aca gac Ser Lys Glu Cys Cys Tyr Gln Ala Arg Gln Asp Lys Lys Lys Thr Asp 610 615 620			1872
10	cga gaa gca gaa cga gga aat cac tat tac cga cag cgt gta tgt gct Arg Glu Ala Glu Arg Gly Asn His Tyr Tyr Arg Gln Arg Val Cys Ala 625 630 635 640			1920
15	gtg tgc ggc aat tcc tat tgg cct aca cac agc caa cag aaa ttc tgc Val Cys Gly Asn Ser Tyr Trp Pro Thr His Ser Gln Gln Lys Phe Cys 645 650 655			1968
20	tcc gaa gaa tgt caa agg gta aat cac aat aag aaa aca ttg gaa ttt Ser Glu Glu Cys Gln Arg Val Asn His Asn Lys Lys Thr Leu Glu Phe 660 665 670			2016
25	tac cac cat aaa aaa gaa aag gag aag ctg caa tgc aaa gat tta tca Tyr His His Lys Lys Glu Lys Glu Lys Leu Gln Cys Lys Asp Leu Ser 675 680 685			2064
30	cag acg aaa gaa cgg gta tcc gat atg aac tta tcg ggg act att act Gln Thr Lys Glu Arg Val Ser Asp Met Asn Leu Ser Gly Thr Ile Thr 690 695 700			2112
35	acc cct gct taa Thr Pro Ala 705			2124
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55	Tyr Leu Glu Asp Tyr Ala Arg Arg Asn Gly Phe Glu Asn Ile Arg His 35 40 45			
60	Phe Thr Asp Asp Gly Phe Ser Gly Val Asn Phe Asn Arg Pro Gly Phe 50 55 60			
65	Gln Ser Leu Ile Lys Glu Val Glu Ala Gly Asn Val Glu Thr Leu Ile 65 70 75 80			
70	Val Lys Asp Met Ser Arg Leu Gly Arg Asn Tyr Leu Gln Val Gly Phe 85 90 95			
75	Tyr Thr Glu Val Leu Phe Pro Gln Lys Asn Val Arg Phe Leu Ala Ile 100 105 110			
80	Asn Asn Ser Ile Asp Ser Asn Asn Ala Ser Asp Asn Asp Phe Ala Pro 115 120 125			
85	Phe Leu Asn Ile Met Asn Glu Trp Tyr Ala Lys Asp Thr Ser Asn Lys 130 135 140			
90	Ile Lys Ala Ile Phe Asp Ala Arg Met Lys Asp Gly Lys Arg Cys Ser 145 150 155 160			

Gly Ser Ile Pro Tyr Gly Tyr Asn Arg Leu Pro Ser Asp Lys Gln Thr
 165 170 175
 5 Leu Val Val Asp Pro Val Ala Ser Glu Val Val Lys Arg Ile Phe Thr
 180 185 190
 Leu Ala Asn Asp Gly Lys Ser Thr Arg Ala Ile Ala Glu Ile Leu Thr
 195 200 205
 10 Glu Glu Lys Val Leu Thr Pro Ala Ala Tyr Ala Lys Glu Tyr His Pro
 210 215 220
 Glu Gln Tyr Asn Gly Asn Lys Phe Thr Asn Pro Tyr Leu Trp Ala Met
 225 230 235 240
 15 Ser Thr Ile Arg Asn Ile Leu Gly Arg Gln Glu Tyr Leu Gly His Thr
 245 250 255
 Val Leu Arg Lys Ser Val Ser Thr Asn Phe Lys Leu His Lys Arg Lys
 20 260 265 270
 Ser Thr Asp Glu Glu Glu Gln Tyr Val Phe Pro Asn Thr His Glu Pro
 275 280 285
 25 Ile Ile Ser Gln Glu Leu Trp Asp Ser Val Gln Lys Arg Arg Ser Arg
 290 295 300
 Val Asn Arg Ala Ser Ala Trp Gly Thr His Ser Asn Arg Leu Ser Gly
 30 305 310 315 320
 Tyr Leu Tyr Cys Ala Asp Cys Gly Arg Arg Met Thr Leu Gln Thr His
 325 330 335
 35 Tyr Ser Lys Lys Asp Gly Ser Val Gln Tyr Ser Tyr Arg Cys Gly Gly
 340 345 350
 Tyr Ala Ser Arg Val Asn Ser Cys Thr Ser His Ser Ile Ser Thr Asp
 355 360 365
 40 Asn Val Glu Ala Leu Ile Leu Ser Ser Val Lys Arg Phe Ser Arg Phe
 370 375 380
 Val Leu Asn Asp Glu Gln Ala Phe Ala Leu Glu Leu Gln Ser Leu Trp
 385 390 395 400
 45 Asn Glu Lys Gln Glu Lys Pro Lys His Asn Gln Ser Glu Leu Gln
 405 410 415
 Arg Cys Gln Lys Arg Tyr Asp Glu Leu Ser Thr Leu Val Arg Gly Leu
 50 420 425 430
 Tyr Glu Asn Leu Met Ser Gly Leu Leu Pro Glu Arg Gln Tyr Lys Gln
 435 440 445
 55 Leu Met Lys Gln Tyr Asp Asp Glu Gln Ala Glu Leu Glu Thr Lys Met
 450 455 460
 Glu Thr Met Lys Thr Glu Leu Ala Glu Glu Lys Val Ser Ser Val Asp
 465 470 475 480
 60 Ile Lys His Phe Ile Ser Leu Ile Arg Lys Cys Lys Asn Pro Thr Glu
 485 490 495
 Ile Ser Asp Thr Met Phe Asn Glu Leu Val Asp Lys Ile Val Val Tyr
 65 500 505 510
 Glu Ala Glu Gly Val Gly Lys Ala Arg Thr Gln Lys Val Asp Ile Tyr

	515	520	525	
	Phe Asn Tyr Val Gly Gln Val Asp Ile Ala Tyr Thr Glu Glu Glu Leu			
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	Ala Glu Ile Glu Thr Gln Lys Glu Gln Glu Gln Gln Arg Leu Ala			
	545	550	555	560
10	Arg Gln Arg Lys Arg Glu Lys Ala Tyr Arg Glu Lys Arg Lys Ala Gln			
	565	570	575	
	Lys Ile Ala Glu Asn Gly Gly Glu Ile Val Lys Thr Lys Val Cys Pro			
	580	585	590	
15	His Cys Asn Lys Glu Phe Ile Pro Thr Ser Asn Arg Gln Val Phe Cys			
	595	600	605	
	Ser Lys Glu Cys Cys Tyr Gln Ala Arg Gln Asp Lys Lys Lys Thr Asp			
	610	615	620	
20	Arg Glu Ala Glu Arg Gly Asn His Tyr Tyr Arg Gln Arg Val Cys Ala			
	625	630	635	640
25	Val Cys Gly Asn Ser Tyr Trp Pro Thr His Ser Gln Gln Lys Phe Cys			
	645	650	655	
	Ser Glu Glu Cys Gln Arg Val Asn His Asn Lys Lys Thr Leu Glu Phe			
	660	665	670	
30	Tyr His His Lys Lys Glu Lys Glu Lys Leu Gln Cys Lys Asp Leu Ser			
	675	680	685	
	Gln Thr Lys Glu Arg Val Ser Asp Met Asn Leu Ser Gly Thr Ile Thr			
	690	695	700	
35	Thr Pro Ala			
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40	<210> 62			
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	Met Gln Asn Gln Gly Gln Asp Lys Tyr Gln Gln Ala Phe Ala Asp Leu			
	1 5 10 15			
55	gag cca ctt tca tct acc gac ggc agt ttt ctc ggc tca agt ctg caa			96
	Glu Pro Leu Ser Ser Thr Asp Gly Ser Phe Leu Gly Ser Ser Leu Gln			
	20 25 30			
60	gca cag cag caa aga gaa cac atg aga aca aaa gta cta caa gac cta			144
	Ala Gln Gln Arg Glu His Met Arg Thr Lys Val Leu Gln Asp Leu			
	35 40 45			
65	gac aag gta aat ctg cgt ttg aag tct gca aag acg aaa gtc tca gtt			192
	Asp Lys Val Asn Leu Arg Leu Lys Ser Ala Lys Thr Lys Val Ser Val			
	50 55 60			
	cga gaa tct aac gga agt ctg caa tta cga gca acg tta cca att aaa			240

	Arg Glu Ser Asn Gly Ser Leu Gln Leu Arg Ala Thr Leu Pro Ile Lys		
65	65	70	75
			80
5	cct gga gat aag gac acc aac ggt aca ggc aga aag caa tac aat ctc Pro Gly Asp Lys Asp Thr Asn Gly Thr Gly Arg Lys Gln Tyr Asn Leu	288	
	85	90	95
10	agc ttg aat atc cct gca aac ttg gat gga ctg aag acg gct gag gaa Ser Leu Asn Ile Pro Ala Asn Leu Asp Gly Leu Lys Thr Ala Glu Glu	336	
	100	105	110
15	gaa gct tat gaa tta ggt aaa tta atc gct cggt aaa acc ttt gaa tgg Glu Ala Tyr Glu Leu Gly Lys Leu Ile Ala Arg Lys Thr Phe Glu Trp	384	
	115	120	125
20	aat gat aaa tat tta ggc aaa gaa gcc act aaa aaa gat tca caa aca Asn Asp Lys Tyr Leu Gly Lys Glu Ala Thr Lys Lys Asp Ser Gln Thr	432	
	130	135	140
25	ata ggt gat tta cta gaa aaa ttt gca gaa gag tat ttt aaa acc cat Ile Gly Asp Leu Leu Glu Lys Phe Ala Glu Glu Tyr Phe Lys Thr His	480	
	145	150	155
	160		
30	aaa cgc acc act aaa agc gaa cat acc ttt ttt tac tat ttt tcc cgc Lys Arg Thr Thr Lys Ser Glu His Thr Phe Phe Tyr Tyr Phe Ser Arg	528	
	165	170	175
35	acc caa cga tat acc aat tcc aaa gat tta gca acg gcg gaa aat ctc Thr Gln Arg Tyr Thr Asn Ser Lys Asp Leu Ala Thr Ala Glu Asn Leu	576	
	180	185	190
40	atc aat tca att gag caa atc gat aaa gaa tgg gcg aga tat aat gcc Ile Asn Ser Ile Glu Gln Ile Asp Lys Glu Trp Ala Arg Tyr Asn Ala	624	
	195	200	205
45	gcc aga gcc ata tca gct ttt tgc ata aca ttc aat ata gaa att gat Ala Arg Ala Ile Ser Ala Phe Cys Ile Thr Phe Asn Ile Glu Ile Asp	672	
	210	215	220
50	ttg tcc cag tat tcc aaa atg cct gat cgc aat tcg cgc aac atc ccc Leu Ser Gln Tyr Ser Lys Met Pro Asp Arg Asn Ser Arg Asn Ile Pro	720	
	225	230	235
	240		
55	ttt gat gca gaa ata cta tca gga att acc aaa ttt gaa gac tat cta Thr Asp Ala Glu Ile Leu Ser Gly Ile Thr Lys Phe Glu Asp Tyr Leu	768	
	245	250	255
60	gtt acc aga gga aat caa gtt aat gaa gat gta aaa gat agc tgg caa Val Thr Arg Gly Asn Gln Val Asn Glu Asp Val Lys Asp Ser Trp Gln	816	
	260	265	270
65	ctt tgg cgc tgg aca tat gga atg tta gca gtt ttt ggt tta cgc ccc Leu Trp Arg Trp Thr Tyr Gly Met Leu Ala Val Phe Gly Leu Arg Pro	864	
	275	280	285
70	agg gaa att ttt att aac cct aat att gat tgg tgg tta agc aaa gag Arg Glu Ile Phe Ile Asn Pro Asn Ile Asp Trp Trp Leu Ser Lys Glu	912	
	290	295	300
75	aat ata gac ctc aca tgg aaa gta gac aaa gaa tgt aaa act ggt gaa Asn Ile Asp Leu Thr Trp Lys Val Asp Lys Glu Cys Lys Thr Gly Glu	960	
	305	310	315
	320		
80	aga caa gca tta ccc tta cat aaa gaa tgg att gat gag ttt gat tta Arg Gln Ala Leu Pro Leu His Lys Glu Trp Ile Asp Glu Phe Asp Leu	1008	
	325	330	335

aga aat ccg aaa tat tta gaa atg ctg gca aca gca att agt aaa aaa Arg Asn Pro Lys Tyr Leu Glu Met Leu Ala Thr Ala Ile Ser Lys Lys 340 345 350	1056
5 gat aaa aca aat cat gct gaa ata aca gcc tta act cag cgt att agt Asp Lys Thr Asn His Ala Glu Ile Thr Ala Leu Thr Gln Arg Ile Ser 355 360 365	1104
10 tgg tgg ttt cgg aaa gtc gaa tta gat ttt aaa ccc tat gat tta cgt Trp Trp Phe Arg Lys Val Glu Leu Asp Phe Lys Pro Tyr Asp Leu Arg 370 375 380	1152
15 cac gcc tgg gca atc aga gcg cat att tta ggc ata cca atc aaa gcg His Ala Trp Ala Ile Arg Ala His Ile Leu Gly Ile Pro Ile Lys Ala 385 390 395 400	1200
20 gcg gct gat aat ttg ggg cat agt atg cag gtt cat aca caa acc tat Ala Ala Asp Asn Leu Gly His Ser Met Gln Val His Thr Gln Thr Tyr 405 410 415	1248
25 cag cgc tgg ttc tcg cta gat atg cgg aag tta gcg att aat cag gct Gln Arg Trp Phe Ser Leu Asp Met Arg Lys Leu Ala Ile Asn Gln Ala 420 425 430	1296
30 ttg act aag agg aat gaa ttt gag gtg att agg gag gag aat gct aaa Leu Thr Lys Arg Asn Glu Phe Glu Val Ile Arg Glu Glu Asn Ala Lys 435 440 445	1344
35 ttg cag ata gaa aat gaa agg ttg agg atg gaa att gag aag tta aag Leu Gln Ile Glu Asn Glu Arg Leu Arg Met Glu Ile Glu Lys Leu Lys 450 455 460	1392
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50 Glu Pro Leu Ser Ser Thr Asp Gly Ser Phe Leu Gly Ser Ser Leu Gln 20 25 30	
55 Ala Gln Gln Gln Arg Glu His Met Arg Thr Lys Val Leu Gln Asp Leu 35 40 45	
60 Asp Lys Val Asn Leu Arg Leu Lys Ser Ala Lys Thr Lys Val Ser Val 50 55 60	
65 Arg Glu Ser Asn Gly Ser Leu Gln Leu Arg Ala Thr Leu Pro Ile Lys 65 70 75 80	
70 Pro Gly Asp Lys Asp Thr Asn Gly Thr Gly Arg Lys Gln Tyr Asn Leu 85 90 95	
75 Ser Leu Asn Ile Pro Ala Asn Leu Asp Gly Leu Lys Thr Ala Glu Glu 100 105 110	
80 Glu Ala Tyr Glu Leu Gly Lys Leu Ile Ala Arg Lys Thr Phe Glu Trp 115 120 125	

Asn Asp Lys Tyr Leu Gly Lys Glu Ala Thr Lys Lys Asp Ser Gln Thr
 130 135 140

5 Ile Gly Asp Leu Leu Glu Lys Phe Ala Glu Glu Tyr Phe Lys Thr His
 145 150 155 160

Lys Arg Thr Thr Lys Ser Glu His Thr Phe Phe Tyr Tyr Phe Ser Arg
 165 170 175

10 Thr Gln Arg Tyr Thr Asn Ser Lys Asp Leu Ala Thr Ala Glu Asn Leu
 180 185 190

15 Ile Asn Ser Ile Glu Gln Ile Asp Lys Glu Trp Ala Arg Tyr Asn Ala
 195 200 205

Ala Arg Ala Ile Ser Ala Phe Cys Ile Thr Phe Asn Ile Glu Ile Asp
 210 215 220

20 Leu Ser Gln Tyr Ser Lys Met Pro Asp Arg Asn Ser Arg Asn Ile Pro
 225 230 235 240

Thr Asp Ala Glu Ile Leu Ser Gly Ile Thr Lys Phe Glu Asp Tyr Leu
 245 250 255

25 Val Thr Arg Gly Asn Gln Val Asn Glu Asp Val Lys Asp Ser Trp Gln
 260 265 270

Leu Trp Arg Trp Thr Tyr Gly Met Leu Ala Val Phe Gly Leu Arg Pro
 275 280 285

30 Arg Glu Ile Phe Ile Asn Pro Asn Ile Asp Trp Trp Leu Ser Lys Glu
 290 295 300

35 Asn Ile Asp Leu Thr Trp Lys Val Asp Lys Glu Cys Lys Thr Gly Glu
 305 310 315 320

Arg Gln Ala Leu Pro Leu His Lys Glu Trp Ile Asp Glu Phe Asp Leu
 325 330 335

40 Arg Asn Pro Lys Tyr Leu Glu Met Leu Ala Thr Ala Ile Ser Lys Lys
 340 345 350

Asp Lys Thr Asn His Ala Glu Ile Thr Ala Leu Thr Gln Arg Ile Ser
 355 360 365

45 Trp Trp Phe Arg Lys Val Glu Leu Asp Phe Lys Pro Tyr Asp Leu Arg
 370 375 380

His Ala Trp Ala Ile Arg Ala His Ile Leu Gly Ile Pro Ile Lys Ala
 385 390 395 400

Ala Ala Asp Asn Leu Gly His Ser Met Gln Val His Thr Gln Thr Tyr
 405 410 415

55 Gln Arg Trp Phe Ser Leu Asp Met Arg Lys Leu Ala Ile Asn Gln Ala
 420 425 430

Leu Thr Lys Arg Asn Glu Phe Glu Val Ile Arg Glu Glu Asn Ala Lys
 435 440 445

60 Leu Gln Ile Glu Asn Glu Arg Leu Arg Met Glu Ile Glu Lys Leu Lys
 450 455 460

65 Met Glu Ile Ala Tyr Lys Asn Ser
 465 470

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 <211> 1008
 <212> DNA
 5 <213> Artificial Sequence

 <220>
 <221> CDS
 10 <222> (1)...(1005)

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 20 gag agg aaa ggg cg^g tat tat gtt tac aag cta gag tat gaa aac ggt 96
 Glu Arg Lys Gly Arg Tyr Tyr Val Tyr Lys Leu Glu Tyr Glu Asn Gly
 20 25 30

 25 gag gta aaa gag cgt tac gt^g ggt cct tta gct gac gtc gtt gaa tca 144
 Glu Val Lys Glu Arg Tyr Val Gly Pro Leu Ala Asp Val Val Glu Ser
 35 40 45

 30 tat cta aaa atg aaa tta ggg gtc gta ggg gat act ccc cta caa gc^g 192
 Tyr Leu Lys Met Lys Leu Gly Val Val Gly Asp Thr Pro Leu Gln Ala
 50 55 60

 35 gat ccc ccc ggt ttc gag ccc ggg aca agc gga agc ggt ggt gga aaa 240
 Asp Pro Pro Gly Phe Glu Pro Gly Thr Ser Gly Ser Gly Gly Lys
 65 70 75 80

 40 gag gga act gaa cga cgt aaa ata gc^g ttg gtt gcc aat ttg cgc caa 288
 Glu Gly Thr Glu Arg Arg Lys Ile Ala Leu Val Ala Asn Leu Arg Gln
 85 90 95

 45 tac gc^g acg gac gg^c aac ata aag gc^g ttc tac aac tat ctc atg aac 336
 Tyr Ala Thr Asp Gly Asn Ile Lys Ala Phe Tyr Asn Tyr Leu Met Asn
 100 105 110

 50 gaa agg ggg ata agc gaa aaa act gca aag gac tac atc aat gct ata 384
 Glu Arg Gly Ile Ser Glu Lys Thr Ala Lys Asp Tyr Ile Asn Ala Ile
 115 120 125

 55 tca aag cc^g tat aaa gag acg aga gac gca cag aag gct tac cga ctc 432
 Ser Lys Pro Tyr Lys Glu Thr Arg Asp Ala Gln Lys Ala Tyr Arg Leu
 130 135 140

 60 ttt gca cgt ttc tta gc^g tca cgc aat atc ata cat gat gaa ttt gc^g 480
 Phe Ala Arg Phe Leu Ala Ser Arg Asn Ile Ile His Asp Glu Phe Ala
 145 150 155 160

 65 gat aaa ata ttg aaa gc^g gta aag gt^g aag aag gc^g aac gct gat atc 528
 Asp Lys Ile Leu Lys Ala Val Lys Val Lys Lys Ala Asn Ala Asp Ile
 165 170 175

 70 tac att cca acg ttg gaa gag ata aaa agg acg tta caa tta gca aaa 576
 Tyr Ile Pro Thr Leu Glu Glu Ile Lys Arg Thr Leu Gln Leu Ala Lys
 180 185 190

 75 gac tat agc gaa aac gtc tac ttc atc tac cgt atc gct ctc gag tc^g 624
 Asp Tyr Ser Glu Asn Val Tyr Phe Ile Tyr Arg Ile Ala Leu Glu Ser
 195 200 205

	ggc gtt agg ctg agc gaa ata ctg aaa gtg ctg aag gaa ccc gaa agg	672		
	Gly Val Arg Leu Ser Glu Ile Leu Lys Val Leu Lys Glu Pro Glu Arg			
210	215	220		
5	gac att tgc ggt aac gac gtc tgt tat tat ccg ctt agt tgg act agg	720		
	Asp Ile Cys Gly Asn Asp Val Cys Tyr Tyr Pro Leu Ser Trp Thr Arg			
225	230	235	240	
10	gga tat aag ggc gtc ttc tat gta ttc cac ata acg cct ctg aag aga	768		
	Gly Tyr Lys Gly Val Phe Tyr Val Phe His Ile Thr Pro Leu Lys Arg			
	245	250	255	
15	gta gag gtg acg aag tgg gca ata gcg gac ttt gaa cga cgt cat aag	816		
	Val Glu Val Thr Lys Trp Ala Ile Ala Asp Phe Glu Arg Arg His Lys			
	260	265	270	
	gac gct ata gcg ata aag tac ttc cgc aaa ttc gta gcg tct aag atg	864		
	Asp Ala Ile Ala Ile Lys Tyr Phe Arg Lys Phe Val Ala Ser Lys Met			
	275	280	285	
20	gct gag cta agc gta ccg tta gat att atc gat ttt att caa ggg cgt	912		
	Ala Glu Leu Ser Val Pro Leu Asp Ile Ile Asp Phe Ile Gln Gly Arg			
	290	295	300	
25	aaa ccg aca cgc gtt tta acg caa cat tac gta tcg ctc ttc ggc ata	960		
	Lys Pro Thr Arg Val Leu Thr Gln His Tyr Val Ser Leu Phe Gly Ile			
	305	310	315	320
30	gcg aaa gag caa tat aaa aag tat gcg gaa tgg cta aaa ggg gtc tga	1008		
	Ala Lys Glu Gln Tyr Lys Tyr Ala Glu Trp Leu Lys Gly Val			
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	<211> 335			
	<212> PRT			
	<213> Artificial Sequence			
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	20 25 30			
	Glu Val Lys Glu Arg Tyr Val Gly Pro Leu Ala Asp Val Val Glu Ser			
	35 40 45			
50	Tyr Leu Lys Met Lys Leu Gly Val Val Gly Asp Thr Pro Leu Gln Ala			
	50 55 60			
55	Asp Pro Pro Gly Phe Glu Pro Gly Thr Ser Gly Ser Gly Gly Lys			
	65 70 75 80			
	Glu Gly Thr Glu Arg Arg Lys Ile Ala Leu Val Ala Asn Leu Arg Gln			
	85 90 95			
60	Tyr Ala Thr Asp Gly Asn Ile Lys Ala Phe Tyr Asn Tyr Leu Met Asn			
	100 105 110			
	Glu Arg Gly Ile Ser Glu Lys Thr Ala Lys Asp Tyr Ile Asn Ala Ile			
	115 120 125			
65.	Ser Lys Pro Tyr Lys Glu Thr Arg Asp Ala Gln Lys Ala Tyr Arg Leu			
	130 135 140			

Phe Ala Arg Phe Leu Ala Ser Arg Asn Ile Ile His Asp Glu Phe Ala
 145 150 155 160

5 Asp Lys Ile Leu Lys Ala Val Lys Val Lys Ala Asn Ala Asp Ile
 165 170 175

Tyr Ile Pro Thr Leu Glu Glu Ile Lys Arg Thr Leu Gln Leu Ala Lys
 180 185 190

10 Asp Tyr Ser Glu Asn Val Tyr Phe Ile Tyr Arg Ile Ala Leu Glu Ser
 195 200 205

Gly Val Arg Leu Ser Glu Ile Leu Lys Val Leu Lys Glu Pro Glu Arg
 15 210 215 220

Asp Ile Cys Gly Asn Asp Val Cys Tyr Tyr Pro Leu Ser Trp Thr Arg
 225 230 235 240

20 Gly Tyr Lys Gly Val Phe Tyr Val Phe His Ile Thr Pro Leu Lys Arg
 245 250 255

Val Glu Val Thr Lys Trp Ala Ile Ala Asp Phe Glu Arg Arg His Lys
 260 265 270

25 Asp Ala Ile Ala Ile Lys Tyr Phe Arg Lys Phe Val Ala Ser Lys Met
 275 280 285

Ala Glu Leu Ser Val Pro Leu Asp Ile Ile Asp Phe Ile Gln Gly Arg
 30 290 295 300

Lys Pro Thr Arg Val Leu Thr Gln His Tyr Val Ser Leu Phe Gly Ile
 305 310 315 320

35 Ala Lys Glu Gln Tyr Lys Lys Tyr Ala Glu Trp Leu Lys Gly Val
 325 330 335

40 <210> 66
 <211> 1441
 <212> DNA
 <213> Artificial Sequence

45 <220>
 <223> Description of Artificial Sequence: DNA sequence
 coding for fusion protein NLS-XisA

50 <220>
 <221> CDS
 <222> (1)..(1437)

<400> 66

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caa caa gcc ttt gca gac tta gag cca ctt tca tct acc gac ggc agt 96
 Gln Gln Ala Phe Ala Asp Leu Glu Pro Leu Ser Ser Thr Asp Gly Ser
 60 20 25 30

ttt ctc ggc tca agt ctg caa gca cag cag caa aga gaa cac atg aga 144
 Phe Leu Gly Ser Ser Leu Gln Ala Gln Gln Gln Arg Glu His Met Arg
 35 40 45

65 aca aaa gta cta caa gac cta gac aag gta aat ctg cgt ttg aag tct 192
 Thr Lys Val Leu Gln Asp Leu Asp Lys Val Asn Leu Arg Leu Lys Ser

50

55

60

	gca aag acg aaa gtc tca gtt cga gaa tct aac gga agt ctg caa tta Ala Lys Thr Lys Val Ser Val Arg Glu Ser Asn Gly Ser Leu Gln Leu 5 65 70 75 80	240
	cga gca acg tta cca att aaa cct gga gat aag gac acc aac ggt aca Arg Ala Thr Leu Pro Ile Lys Pro Gly Asp Lys Asp Thr Asn Gly Thr 10 85 90 95	288
	ggc aga aag caa tac aat ctc agc ttg aat atc cct gca aac ttg gat Gly Arg Lys Gln Tyr Asn Leu Ser Leu Asn Ile Pro Ala Asn Leu Asp 15 100 105 110	336
	gga ctg aag acg gct gag gaa gaa gct tat gaa tta ggt aaa tta atc Gly Leu Lys Thr Ala Glu Glu Ala Tyr Glu Leu Gly Lys Leu Ile 15 115 120 125	384
10	gct cggtt aaaa acc ttt gaa tgg aat gat aaaa tat tta ggc aaaa gaa gcc Ala Arg Lys Thr Phe Glu Trp Asn Asp Lys Tyr Leu Gly Lys Glu Ala 10 130 135 140	432
15	act aaaa aaaa gat tca caa aca ata ggt gat tta cta gaa aaaa ttt gca Thr Lys Lys Asp Ser Gln Thr Ile Gly Asp Leu Leu Glu Lys Phe Ala 15 145 150 155 160	480
20	gaa gag tat ttt aaaa acc cat aaaa cgc acc act aaaa agc gaa cat acc Glu Glu Tyr Phe Lys Thr His Lys Arg Thr Thr Lys Ser Glu His Thr 20 165 170 175	528
25	ttt ttt tac tat ttt tcc cgc acc caa cga tat acc aat tcc aaaa gat Phe Phe Tyr Tyr Phe Ser Arg Thr Gln Arg Tyr Thr Asn Ser Lys Asp 25 180 185 190	576
30	tta gca acg gcg gaa aat ctc atc aat tca att gag caa atc gat aaaa Leu Ala Thr Ala Glu Asn Leu Ile Asn Ser Ile Glu Gln Ile Asp Lys 30 195 200 205	624
35	gaa tgg gcg aga tat aat gcc gcc aga gcc ata tca gct ttt tgc ata Glu Trp Ala Arg Tyr Asn Ala Ala Arg Ala Ile Ser Ala Phe Cys Ile 35 210 215 220	672
40	aca ttc aat ata gaa att gat ttg tcc cag tat tcc aaaa atg cct gat Thr Phe Asn Ile Glu Ile Asp Leu Ser Gln Tyr Ser Lys Met Pro Asp 40 225 230 235 240	720
45	cgc aat tcg cgc aac atc ccc aca gat gca gaa ata cta tca gga att Arg Asn Ser Arg Asn Ile Pro Thr Asp Ala Glu Ile Leu Ser Gly Ile 45 245 250 255	768
50	acc aaa ttt gaa gac tat cta gtt acc aga gga aat caa gtt aat gaa Thr Lys Phe Glu Asp Tyr Leu Val Thr Arg Gly Asn Gln Val Asn Glu 50 260 265 270	816
55	gat gta aaa gat agc tgg caa ctt tgg cgc tgg aca tat gga atg tta Asp Val Lys Asp Ser Trp Gln Leu Trp Arg Trp Thr Tyr Gly Met Leu 55 275 280 285	864
60	gca gtt ttt ggt tta cgc ccc agg gaa att ttt att aac cct aat att Ala Val Phe Gly Leu Arg Pro Arg Glu Ile Phe Ile Asn Pro Asn Ile 60 290 295 300	912
65	gat tgg tgg tta agc aaa gag aat ata gac ctc aca tgg aaaa gta gac Asp Trp Trp Leu Ser Lys Glu Asn Ile Asp Leu Thr Trp Lys Val Asp 65 305 310 315 320	960
	aaa gaa tgt aaa act ggt gaa aga caa gca tta ccc tta cat aaaa gaa	1008

Lys Glu Cys Lys Thr Gly Glu Arg Gln Ala Leu Pro Leu His Lys Glu
 325 330 335

5 tgg att gat gag ttt gat tta aga aat ccg aaa tat tta gaa atg ctg 1056
 Trp Ile Asp Glu Phe Asp Leu Arg Asn Pro Lys Tyr Leu Glu Met Leu
 340 345 350

10 gca aca gca att agt aaa aaa gat aaa aca aat cat gct gaa ata aca 1104
 Ala Thr Ala Ile Ser Lys Lys Asp Lys Thr Asn His Ala Glu Ile Thr
 355 360 365

15 gcc tta act cag cgt att agt tgg tgg ttt cgg aaa gtc gaa tta gat 1152
 Ala Leu Thr Gln Arg Ile Ser Trp Trp Phe Arg Lys Val Glu Leu Asp
 370 375 380

20 ttt aaa ccc tat gat tta cgt cac gcc tgg gca atc aga gcg cat att 1200
 Phe Lys Pro Tyr Asp Leu Arg His Ala Trp Ala Ile Arg Ala His Ile
 385 390 395 400

25 tta ggc ata cca atc aaa gcg gcg gct gat aat ttg ggg cat agt atg 1248
 Leu Gly Ile Pro Ile Lys Ala Ala Asp Asn Leu Gly His Ser Met
 405 410 415

30 cag gtt cat aca caa acc tat cag cgc tgg ttc tcg cta gat atg cgg 1296
 Gln Val His Thr Gln Thr Tyr Gln Arg Trp Phe Ser Leu Asp Met Arg
 420 425 430

35 aag tta gcg att aat cag gct ttg act aag agg aat gaa ttt gag gtg 1344
 Lys Leu Ala Ile Asn Gln Ala Leu Thr Lys Arg Asn Glu Phe Glu Val
 435 440 445

40 att agg gag gag aat gct aaa ttg cag ata gaa aat gaa agg ttg agg 1392
 Ile Arg Glu Glu Asn Ala Lys Leu Gln Ile Glu Asn Glu Arg Leu Arg
 450 455 460

45 atg gaa att gag aag tta aag atg gaa ata gct tat aag aat agt tgag 1441
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 465 470 475

50 <210> 67
 <211> 479
 <212> PRT
 45 <213> Artificial Sequence
 <223> Description of Artificial Sequence: DNA sequence
 coding for fusion protein NLS-XisA

55 <400> 67
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Gln Gln Ala Phe Ala Asp Leu Glu Pro Leu Ser Ser Thr Asp Gly Ser
 20 25 30

60 Thr Lys Val Leu Gln Asp Leu Asp Lys Val Asn Leu Arg Leu Lys Ser
 50 55 60

Ala Lys Thr Lys Val Ser Val Arg Glu Ser Asn Gly Ser Leu Gln Leu
 65 70 75 80

65 Arg Ala Thr Leu Pro Ile Lys Pro Gly Asp Lys Asp Thr Asn Gly Thr
 85 90 95

Gly Arg Lys Gln Tyr Asn Leu Ser Leu Asn Ile Pro Ala Asn Leu Asp

	100	105	110
	Gly Leu Lys Thr Ala Glu Glu Ala Tyr Glu Leu Gly Lys Leu Ile		
5	115	120	125
	Ala Arg Lys Thr Phe Glu Trp Asn Asp Lys Tyr Leu Gly Lys Glu Ala		
	130	135	140
10	Thr Lys Lys Asp Ser Gln Thr Ile Gly Asp Leu Leu Glu Lys Phe Ala		
	145	150	155
	Glu Glu Tyr Phe Lys Thr His Lys Arg Thr Thr Lys Ser Glu His Thr		
	165	170	175
15	Phe Phe Tyr Tyr Phe Ser Arg Thr Gln Arg Tyr Thr Asn Ser Lys Asp		
	180	185	190
	Leu Ala Thr Ala Glu Asn Leu Ile Asn Ser Ile Glu Gln Ile Asp Lys		
	195	200	205
20	Glu Trp Ala Arg Tyr Asn Ala Ala Arg Ala Ile Ser Ala Phe Cys Ile		
	210	215	220
	Thr Phe Asn Ile Glu Ile Asp Leu Ser Gln Tyr Ser Lys Met Pro Asp		
25	225	230	235
	Arg Asn Ser Arg Asn Ile Pro Thr Asp Ala Glu Ile Leu Ser Gly Ile		
	245	250	255
30	Thr Lys Phe Glu Asp Tyr Leu Val Thr Arg Gly Asn Gln Val Asn Glu		
	260	265	270
	Asp Val Lys Asp Ser Trp Gln Leu Trp Arg Trp Thr Tyr Gly Met Leu		
	275	280	285
35	Ala Val Phe Gly Leu Arg Pro Arg Glu Ile Phe Ile Asn Pro Asn Ile		
	290	295	300
	Asp Trp Trp Leu Ser Lys Glu Asn Ile Asp Leu Thr Trp Lys Val Asp		
40	305	310	315
	Lys Glu Cys Lys Thr Gly Glu Arg Gln Ala Leu Pro Leu His Lys Glu		
	325	330	335
45	Trp Ile Asp Glu Phe Asp Leu Arg Asn Pro Lys Tyr Leu Glu Met Leu		
	340	345	350
	Ala Thr Ala Ile Ser Lys Lys Asp Lys Thr Asn His Ala Glu Ile Thr		
	355	360	365
50	Ala Leu Thr Gln Arg Ile Ser Trp Trp Phe Arg Lys Val Glu Leu Asp		
	370	375	380
	Phe Lys Pro Tyr Asp Leu Arg His Ala Trp Ala Ile Arg Ala His Ile		
55	385	390	395
	Leu Gly Ile Pro Ile Lys Ala Ala Asp Asn Leu Gly His Ser Met		
	405	410	415
60	Gln Val His Thr Gln Thr Tyr Gln Arg Trp Phe Ser Leu Asp Met Arg		
	420	425	430
	Lys Leu Ala Ile Asn Gln Ala Leu Thr Lys Arg Asn Glu Phe Glu Val		
	435	440	445
65	Ile Arg Glu Glu Asn Ala Lys Leu Gln Ile Glu Asn Glu Arg Leu Arg		
	450	455	460

Met Glu Ile Glu Lys Leu Lys Met Glu Ile Ala Tyr Lys Asn Ser
465 470 475

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<210> 68
<211> 1029

<212> DNA

10 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence coding for fusion protein NLS-Ssv

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tac ggg gat tat att tta cgc gag agg aaa ggg cg_g tat tat gtt tac 96
 Tyr Gly Asp Tyr Ile Leu Arg Glu Arg Lys Gly Arg Tyr Tyr Val Tyr
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10

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aag cta gag tat gaa aac ggt gag gta aaa gag cgt tac gtg ggt cct 144
Lys Leu Tyr Glu Asn Gly Glu Val Lys Glu Arg Tyr Val Gly Pro
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10

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 Leu Ala Asp Val Val Glu Ser Tyr Leu Lys Met Lys Leu Gly Val Val
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40

agc gga agc ggt ggt gga aaa gag gga act gaa cga cgt aaa ata gcg 288
 Ser Gly Ser Gly Gly Lys Glu Gly Thr Glu Arg Arg Lys Ile Ala
 85 90 95

45

ttg gtt gcc aat ttg cgccaa tac gcg acg gac ggc aac ata aag gcg 336
Leu Val Ala Asn Leu Arg Gln Thr Ala Thr Asn Glu Asp Ile

100	105	110
tac aac tat ctc atg aac gaa agg ggg ata agc gaa aaa act gca		384
Phe Tyr Asn Tyr Leu Met Asn Glu Arg Gly Ile Ser Glu Lys Thr Ala		
115	120	125

aag gac tac atc aat gct ata tca aag ccg tat aaa gag acg aqa qac 432

55

gca cag aag gct tac cga ctc ttt gca cgt ttc tta qcq tca cgc aat 480

60

65

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aag aag gcg aac gct gat atc tac att cca acg ttg gaa gag ata aaa      576
Lys Lys Ala Asn Ala Asp Ile Tyr Ile Pro Thr Leu Glu Glu Ile Lys
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	tac cgt atc gct ctc gag tcg ggc gtt agg ctg agc gaa ata ctg aaa	672
	Tyr Arg Ile Ala Leu Glu Ser Gly Val Arg Leu Ser Glu Ile Leu Lys	
	210 215 220	
10	gtg ctg aag gaa ccc gaa agg gac att tgc ggt aac gac gtc tgt tat	720
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	cac ata acg cct ctg aag aga gta gag gtg acg aag tgg gca ata gcg	816
	His Ile Thr Pro Leu Lys Arg Val Glu Val Thr Lys Trp Ala Ile Ala	
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5	tac gta tcg ctc ttc ggc ata gcg aaa gag caa tat aaa aag tat gcg	1008
	Tyr Val Ser Leu Phe Gly Ile Ala Lys Glu Gln Tyr Lys Lys Tyr Ala	
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	35 40 45	
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65	Ser Gly Ser Gly Gly Lys Glu Gly Thr Glu Arg Arg Lys Ile Ala	
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5 Phe Tyr Asn Tyr Leu Met Asn Glu Arg Gly Ile Ser Glu Lys Thr Ala
 115 120 125

Lys Asp Tyr Ile Asn Ala Ile Ser Lys Pro Tyr Lys Glu Thr Arg Asp
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10 Ala Gln Lys Ala Tyr Arg Leu Phe Ala Arg Phe Leu Ala Ser Arg Asn
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15 Ile Ile His Asp Glu Phe Ala Asp Lys Ile Leu Lys Ala Val Lys Val
 165 170 175

Lys Lys Ala Asn Ala Asp Ile Tyr Ile Pro Thr Leu Glu Glu Ile Lys
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20 Arg Thr Leu Gln Leu Ala Lys Asp Tyr Ser Glu Asn Val Tyr Phe Ile
 195 200 205

Tyr Arg Ile Ala Leu Glu Ser Gly Val Arg Leu Ser Glu Ile Leu Lys
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25 Val Leu Lys Glu Pro Glu Arg Asp Ile Cys Gly Asn Asp Val Cys Tyr
 225 230 235 240

Tyr Pro Leu Ser Trp Thr Arg Gly Tyr Lys Gly Val Phe Tyr Val Phe
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His Ile Thr Pro Leu Lys Arg Val Glu Val Thr Lys Trp Ala Ile Ala
 260 265 270

Asp Phe Glu Arg Arg His Lys Asp Ala Ile Ala Ile Lys Tyr Phe Arg
 275 280 285

Lys Phe Val Ala Ser Lys Met Ala Glu Leu Ser Val Pro Leu Asp Ile
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40 Ile Asp Phe Ile Gln Gly Arg Lys Pro Thr Arg Val Leu Thr Gln His
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 55 <213> Artificial Sequence

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10 <213> Artificial Sequence

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 pBS-SSVs

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55 <220>
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15 <220>
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45 <210> 94
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